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(54) **METHOD FOR QUALITY CONTROL OF AN ATTENUATED VARICELLA LIVE VACCINE**

VERFAHREN ZUM KONTROLLIEREN DER QUALITÄTEN EINES ABGESCHWÄCHTEN
VARICELLA PHASEN-IMPfstOFFES

PROCEDE DE CONTROLE DES QUALITES D'UN VACCIN DE PHASE ATTENUE DE VARICELLE

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Description**BACKGROUND OF THE INVENTION****Field of the Invention**

[0001] The present invention relates to a method for quality control of an attenuated varicella live vaccine. More particularly, the present invention relates to a method for quality control of an attenuated varicella live vaccine, which comprises subjecting the genomic DNA of a sample varicella vaccine virus to sequence analysis and confirming that the genomic DNA of the sample varicella vaccine virus conserves the specific nucleotides without suffering mutation. By the use of the method of the present invention, it has become possible to determine very accurately the qualification of an attenuated varicella virus as an active ingredient of an attenuated varicella live vaccine and, consequently, to conduct an exact quality control of the vaccines.

Prior Art

[0002] As is well known, attenuated varicella live vaccines used today are produced from a seed strain of varicella virus which is derived from the attenuated varicella virus Oka strain (see Examined Japanese Patent Application Publication No. 53-41202 and U.S. Patent No. 3,985,615), and the attenuated live vaccines are used widely throughout the world (Requirements for Varicella Vaccine (Live) Adopted 1984; Revised 1993: WHO Technical Report Series, No. 848, pp. 22-38, 1994). To ensure the safety and effectiveness of the vaccine, the number of passages of a virus used for producing the vaccine is restricted under the control of a seed lot system, taking into consideration the potential genetic mutation which is likely to occur during the passage. That is, the manufacturers are under an obligation to produce varicella vaccines only from the virus derived from the approved seed virus for the live varicella vaccine, wherein the number of passages of the virus is not more than 10 as counted from the approved seed virus which is counted as 0 passage. In other words, the quality control and quality assurance of the attenuated varicella live vaccine rely upon the fulfillment of the seed lot system by the manufacturers, and such a method for the quality control and quality assurance is not a method which can be traced and analyzed by a person skilled in the art.

[0003] Further, from the viewpoint of epidemiology which involves a tracing of the effects of the varicella vaccine and a post-market surveillance (PMS), the virological difference between the fresh wild-type strains isolated from the naturally infected varicella patients and the vaccine virus strains derived from the above-mentioned Oka strain needs to be determined, and various analyses, such as those utilizing immunological techniques and genetic engineering techniques, have been attempted for determination of the virological difference. For example, the following analyses have been reported: the difference in DNA sequence between the various VZV strains (Journal of Virology, 59, 660-668, 1986; and Journal of General Virology, 67, 1759-1816, 1986), the difference in the absence or presence of a restriction enzyme *Pst* I cleavage site (Japanese Journal of Experimental Medicine, 59, 233-237, 1989), the difference in RFLP (restriction fragment length polymorphism) of the PCR (polymerase chain reaction) product (Journal of Virology, 66, 1016-1020, 1992), and the difference in the absence or presence of a restriction enzyme *Pst* I restriction site which is taken in combination with the difference in RFLP of the PCR product (Journal of Clinical Microbiology, 33, 658-660, 1995). However, all of these analyses only propose criteria which can be used for differentiating a fresh wild-type strain from a vaccine strain derived from the Oka strain, and such analyses lack reliability and exactness. In addition, a method for identifying the attenuated varicella virus Oka strain by using gene 14 region (U.S. Patent No. 6,093,535) and a method for identifying the attenuated varicella live vaccine virus by using gene 62 region (International Patent Application Publication No. , WO 00/50603) have been known. Both of these methods enabled a determination of the differences among the varicella virus Oka strain (virulent parental strain), a vaccine strain derived therefrom (attenuated Oka strain) and a varicella virus strain other than the Oka strain, but neither of these methods was satisfactory as a standard for the quality control and quality assurance of the attenuated varicella live vaccine.

[0004] As mentioned above, at present, the quality of the attenuated varicella virus used as an active ingredient of an attenuated varicella live vaccine is controlled by the fulfillment of the seed lot system by the manufacturers. In other words, a method which can be traced and analyzed by a third party for evaluating and confirming the effectiveness of the vaccine, such as a method utilizing a direct and quantitative genetic analysis of the genomic DNA of a seed virus or a vaccine virus, has not been used for the quality control of the vaccine and, thus, the exactness of the quality control is incomputable and vague. Therefore, an improvement in the exactness of the quality control and quality assurance is critically important for assuring the effectiveness, safety and uniformity of the attenuated varicella live vaccine. However, as mentioned above, a reliable method for the quality control has not been established, and a development of such a method has been earnestly desired in the art.

SUMMARY OF THE INVENTION

[0005] In the above situation, the present inventors have made extensive and intensive studies with a view toward developing a novel method for accurately and quantitatively conducting the quality control of an attenuated varicella live vaccine. Specifically, the present inventors determined the whole genomic nucleotide sequence of the attenuated varicella virus Oka strain containing more than 120,000 nucleotides, conducted a comparative analysis between the determined nucleotide sequence of the attenuated Oka strain and the whole genomic nucleotide sequences of the virulent strain and the parental Oka strain (virulent strain), and identified the genetic mutations of the attenuated varicella virus Oka strain. As a result, they have found that, by evaluating and determining whether or not a varicella virus strain conserves the below-mentioned specific nucleotides, a virus strain conserving the specific nucleotides can be determined accurately as a virus strain capable of functioning as an attenuated varicella vaccine virus. The present invention has been completed, based on this novel finding.

[0006] Therefore, it is an object of the present invention to provide a novel method for the quality control of an attenuated varicella live vaccine.

[0007] The foregoing and other objects, features and advantages of the present invention will be apparent to those skilled in the art from the following detailed description and the appended claims taken in connection with the accompanying sequence listing and drawings.

SEQUENCE LISTING FREE TEXT

[0008]

SEQ ID NOs: 3 and 4 are of PCR primers used for detecting a mutation of the 560th nucleotide of a varicella vaccine virus.

SEQ ID NOs: 5 and 6 are of PCR primers used for detecting a mutation of the 5,745th nucleotide of a varicella vaccine virus.

SEQ ID NOs: 7 and 8 are of PCR primers used for detecting a mutation of the 26,125th nucleotide of a varicella vaccine virus.

SEQ ID NOs: 9 and 10 are of PCR primers used for detecting a mutation of the 94,167th nucleotide of a varicella vaccine virus.

SEQ ID NOs: 11 and 12 are of PCR primers used for detecting mutations of the 105,356th, 105,544th, 124,353rd and 124,541st nucleotides of a varicella vaccine virus.

SEQ ID NOs: 13 and 14 are of PCR primers used for detecting mutations of the 105,705th, 106,262nd, 123,635th and 124,192nd nucleotides of a varicella vaccine virus.

SEQ ID NOs: 15 and 16 are of PCR primers used for detecting mutations of the 107,136th, 107,252nd, 122,645th and 122,761st nucleotides of a varicella vaccine virus.

SEQ ID NOs: 17 and 18 are of PCR primers used for detecting mutations of the 108,111st and 121,786th nucleotides of a varicella vaccine virus.

BRIEF DESCRIPTION OF THE DRAWINGS

[0009] In the drawings:

Fig. 1 is a genetic map of the varicella virus Oka strain showing the number and direction of each gene, wherein, ▽ represents a synonymous substitution, ▼ represents a nonsynonymous substitution, V represents a mutation in a noncoding region, O represents deletion or insertion, the genome length is shown every 20 kb, R1 to R4 represent repetitive sequences, Ori represents an origin of replication, TRL represents a "Terminal Repeat Long", UL represents a "Unique Long", IRL represents an "Internal Repeat Long", IRS represents an "Internal Repeat Short", US represents a "Unique Short", and TRS represents a "Terminal Repeat Short"; and wherein the nucleotide sequence of gene 62 to gene 64 and the nucleotide sequence of gene 69 to gene 71 are symmetrical to each other (i.e., the two nucleotide sequences are inverted repeats); and

Fig. 2 shows the electropherograms which are the results of the RFLP analyses conducted in Example 4, wherein, the restriction enzymes used for treating the PCR products are as follows: Fig. 2(a) was obtained using Nla III, Fig. 2(b) was obtained using Alu I, Fig. 2(c) was obtained using BstX I, Fig. 2(d) was obtained using SfaN I, Fig. 2(e) was obtained using Acc II, Fig. 2(f) was obtained using Sac II, Fig. 2(g) was obtained using Sma I, Fig. 2(h) was obtained using BssH II and Nae I in combination, and Fig. 2(h) was obtained using Bsr I; and wherein, V represents the attenuated Oka strain, P represents the parental Oka strain, and K represents the Kawaguchi strain.

[0010] The terminologies used in the present specification are defined in the following items (a) to (g).

(a) VZV: A virus which causes varicella and herpes zoster. "VZV" is an abbreviation for "varicella-zoster virus" which is frequently referred to simply as "varicella virus".

(b) Varicella vaccine virus and varicella vaccine: A varicella vaccine virus is an active ingredient of a vaccine and it is an attenuated virus. A varicella vaccine is a vaccine effective for preventing the infection with a VZV or the onset of the disease after the infection.

(c) Attenuated Oka strain: Attenuated Oka strain is the attenuated varicella virus Oka strain (see Examined Japanese Patent Application Publication 53-41202 and U.S. Patent No. 3,985,615) or an attenuated varicella virus derived therefrom. The attenuated Oka strain is deposited under the deposition number VR-795 on March 14, 1975 with ATCC.

(d) Parental Oka strain: Parental Oka strain is the originally isolated, wild-type (virulent) varicella virus Oka strain.

(e) Quality control: For assuring the effectiveness, safety and uniformity of a vaccine, raw materials for a vaccine, intermediates obtained during the production of a vaccine, and final products are subjected to various tests or analyses for confirming and assuring their qualification as a vaccine. With respect to an attenuated varicella live vaccine, at present, the quality control of the vaccine is conducted in accordance with Pharmaceutical Affairs Law (the Law No. 145 established in 1960), Article 42, Item 1 and a provision entitled "Dried Attenuated Varicella Virus Live Vaccine" in the Notification No. 217 of the Japanese Ministry of Health and Welfare: Seibutsugakuteki Seizai Kijun (Minimum Requirements for Biological Products) or the above-mentioned "Requirements for Varicella Vaccine (Live)" of WHO.

(f) Nucleotide number of a DNA sequence: In the present invention, all nucleotide numbers of the varicella viruses are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain (Journal of General Virology, 67, 1759-1816, 1986 and GenBank (National Center for Biotechnology Information, National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA), Accession No. X04370) which is shown in SEQ ID NO: 1. Further, in the present invention, the nucleotide sequences are the sequences of a sense strand unless otherwise specified.

(g) DNA mutation: Mutations in the genomic DNA of the attenuated Oka strain were identified by conducting homology searches among the nucleotide sequences of the attenuated Oka strain, the Dumas strain and the virulent parental Oka strain. For example, the DNA mutation is described as follows: "The nucleotide A which is the 5,745th nucleotide of the Dumas strain and a nucleotide at a corresponding site of the parental Oka strain has been mutated to G in the attenuated Oka strain. This nucleotide mutation is a nonsynonymous substitution in which Ser is replaced with Pro."

DETAILED DESCRIPTION OF THE INVENTION

[0011] In an aspect of the present invention, there is provided an accurate method for the quality control of an attenuated varicella live vaccine.

[0012] For easy understanding of the present invention, the essential features and various embodiments of the present invention are enumerated below.

1. A method for the quality control of an attenuated varicella live vaccine, which comprises subjecting the genomic DNA of a sample varicella vaccine virus to sequence analysis and confirming that the genomic DNA of the sample varicella vaccine virus conserves without suffering mutation the following 5 nucleotides:

the 5,745th G, the 105,356th C, the 105,544th G, the 106,262nd C and the 107,252nd C,

wherein the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

2. The method according to item 1 above, wherein the conservation of the 5 nucleotides combination is confirmed by an RFLP analysis using the following primers:

a pair of primers of SEQ ID NOs: 5 and 6 with respect to the confirmation of the 5,745th G;

a pair of primers of SEQ ID NOs: 11 and 12 with respect to the confirmation of the 105,356th C and the 105,544th G;

a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 106,262nd C; and

a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 107,252nd C.

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3. The method according to item 1 or 2 above, which further comprises confirming that the the genomic DNA of sample varicella vaccine virus conserves without suffering mutation the following 4 nucleotides:

the 122,645th G, the 123,635th G, the 124,353rd C and the 124,541st G,

wherein the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

4. The method according to item 3 above, wherein the conservation of the 4 nucleotides is confirmed by an RFLP analysis using the following primers:

a pair of primers of SEQ ID NOs: 11 and 12 with respect to the confirmation of the 124,353rd C and the 124,541st G;

a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 123,635th G; and

a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 122,645th G.

5. The method according to any one of items 1 to 4 above, which further comprises confirming that the genomic DNA of the sample varicella vaccine virus conserves without suffering mutation the following 49 nucleotides:

the 560th C, the 703rd Y, the 763rd Y, the 2,515th Y, the 10,900th Y, the 12,779th Y, the 19,431st Y, the 26,125th G, the 31,732nd Y, the 38,036th Y, the 39,227th K, the 58,595th R, the 59,287th R, the 64,067th R, the 71,252nd Y, the 82,225th R, the 84,091st R, the 87,280th R, the 87,306th Y, the 89,734th R, the 90,535th R, the 94,167th C, the 97,748th R, the 97,796th Y, the 101,089th R, the 105,169th R, the 105,310th R, the 105,705th C, the 106,710th R, the 107,136th C, the 107,599th R, the 107,797th R, the 108,111st C, the 108,838th R, the 109,137th R, the 109,200th R, the 111,650th R, the 118,247th Y, the 120,697th Y, the 120,760th Y, the 121,059th Y, the 121,786th G, the 122,100th Y, the 122,298th Y, the 122,761st G, the 123,187th Y, the 124,192nd G, the 124,587th Y and the 124,728th Y,

wherein:

the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1,

R represents A or G,

Y represents C or T, and

K represents G or T.

6. The method according to item 5 above, wherein the conservation of the 560th C, the 26,125th G, the 94,167th C, the 105,705th C, the 107,136th C, the 108,111st C, the 121,786th G, the 122,761st G and the 124,192nd G among the 49 nucleotides is confirmed by an RFLP analysis using the following primers:

a pair of primers of SEQ ID NOs: 3 and 4 with respect to the confirmation of the 560th C;

a pair of primers of SEQ ID NOs: 7 and 8 with respect to the confirmation of the 26,125th G;

a pair of primers of SEQ ID NOs: 9 and 10 with respect to the confirmation of the 94,167th C;

a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 105,705th C and the 124,192nd G;

a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 107,136th C and the 122,761st G; and

a pair of primers of SEQ ID NOs: 17 and 18 with respect to the confirmation of the 108,111st C and the 121,786th G.

7. The method according to any one of items 1 to 6 above, which further comprises confirming deletion mutations in two origins of replication of the genomic DNA of the sample varicella vaccine virus, wherein the two origins of replication are a region corresponding to the 110,087th to 110,350th nucleotides of the sense strand of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1 and a region corresponding to the 119,547th to 119,810th nucleotides of the genomic DNA of the antisense strand of the Dumas strain, and wherein the deletion mutations occur with respect to segments each having a nucleotide sequence of ATATATATA arranged in the direction of from the 5' end to the 3' end, the segments being a segment corresponding to the 110,219th to 110,227th nucleotides of the genomic DNA of the sense strand of the Dumas strain and a segment

corresponding to the 119,670th to 119,678th nucleotides of the antisense strand of the genomic DNA of the Dumas strain.

8. The method according to any one of items 1 to 7 above, which further comprises confirming that the repetitive sequence of one whole R1 region of the genomic DNA of the sample varicella vaccine virus is a nucleotide sequence of abbabba'bbb'abababx arranged in the direction of from the 5' end to the 3' end, wherein:

a represents a nucleotide sequence of

GGACGCGATCGACGACGA;

a' represents a nucleotide sequence of

GGACGCGATTGACGACGA;

b represents a nucleotide sequence of

GGGAGAGGCGGAGGA;

b' represents a nucleotide sequence of

GGACGCGGCGGAGGA; and

x represents a nucleotide sequence of GGA,

wherein the whole R1 region is a region corresponding to the 13,937th to 14,242nd nucleotides of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

9. The method according to any one of items 1 to 8 above, which further comprises confirming that the repetitive sequence of each of two whole R4 regions of the genomic DNA of the sample varicella vaccine virus is a nucleotide sequence of aaaaaaaaaaax arranged in the direction of from the 5' end to the 3' end, wherein:

a represents a nucleotide sequence of

CCCCGCCGATGGGGAGGGGCGCGGTA; and

x represents a nucleotide sequence of

CCCCGCCGATG,

wherein the two whole R4 regions are a region corresponding to the 109,762nd to 109,907th nucleotides of the sense strand of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1 and a region corresponding to the 119,990th to 120,135th nucleotides of the genomic DNA of the antisense strand of the Dumas strain.

[0013] The present invention is described in detail below.

[0014] During the course of studies for completing the method of the present invention, the present inventors determined for the first time the whole nucleotide sequence of the genomic DNA of the attenuated Oka strain (deposited under the deposition number VR-795 on March 14, 1975 with ATCC (American Type Culture Collection; 10801 University Boulevard, Manassas, VA 20110-2209, USA)). This sequence is shown in SEQ ID NO:2. Further, using the determined whole genomic DNA sequence of the attenuated Oka strain, the present inventors conducted a homology search among the whole genomic DNA sequences of the Dumas strain, the parental Oka strain and the attenuated Oka strain. As a result, the present inventors disclosed the nucleotide mutations of the attenuated Oka strain (i.e., the nucleotides of the attenuated Oka strain which are different from the nucleotides of the Dumas strain and/or the parental Oka strain at the corresponding sites) shown in Table 1 below. The present inventors made further analyses of the nucleotide mutations and identified the synonymous substitutions (no amino acid replacement resulting from the nucleotide mutations) and nonsynonymous substitutions (amino acid replacements resulting from the nucleotide mutations); mutations in noncoding

regions (ncr mutation); stop codon mutations (ochre/amber mutation); number of repetitions and the sequence size of the repetitive sequences and the differences in the order of the repetitions; and mutations in the origins of replication (inverted repeats; see Fig. 1). As explained in detail below, the mutations of the attenuated Oka strain which have been disclosed by the present inventors are useful for differentiating the attenuated Oka strain from other varicella virus strains, especially from the virulent strains and, therefore, these mutations can be used for the quality control of the attenuated varicella live vaccine.

[0015] Among the nucleotide mutations of the attenuated Oka strain shown in Table 1, the important mutations show the XXY pattern or the XX(X/Y) pattern. The mutation showing the XXY pattern is a mutation wherein a nucleotide of the parental Oka strain is identical to a corresponding nucleotide of the Dumas strain (that is, both nucleotides are "X"), but the corresponding nucleotide of the attenuated Oka strain is a mutated nucleotide (that is, the nucleotide is mutated to "Y"). Such a mutation is unique to the attenuated Oka strain. The mutation showing the XX(X/Y) pattern is a mutation wherein a nucleotide of the parental Oka strain is identical to a corresponding nucleotide of the Dumas strain (that is, both nucleotides are "X"), but a corresponding nucleotide of the attenuated Oka strain is a mixture of a nucleotide which is identical to that of the Dumas strain and a mutated nucleotide (that is, the mixture of the identical nucleotide "X" and the mutated nucleotide "Y"). In the genome of the attenuated Oka strain, there are 18 nucleotide mutations showing the XXY pattern and 40 nucleotide mutations showing the XX(X/Y) pattern. Among the total of 58 nucleotide mutations, 49 nucleotide mutations are found in the coding regions, 8 nucleotide mutations are found in the noncoding regions, and 1 nucleotide mutation is found in a stop codon. Further, among the 49 nucleotide mutations in the coding regions, 29 nucleotide mutations are nonsynonymous substitutions, and 20 nucleotide mutations are synonymous substitutions. Further detailed analyses revealed that among the 18 nucleotide mutations showing the XXY pattern, 9 nucleotide mutations are nonsynonymous substitutions, 8 nucleotide mutations are synonymous substitutions, and 1 nucleotide mutation is found in a noncoding region. The following nucleotide mutations which show the XXY pattern and are nonsynonymous substitutions are unique to the attenuated Oka strain: the 5,745th G of gene 6; the 105,356th C, 105,544th G, 106,262nd C and 107,252nd C of gene 62; and the 122,645th G, 123,635th G, 124,353rd C and 124,541st G of gene 71. These unique nucleotides of the attenuated Oka strain are considered to be closely related to the attenuation and safety of a varicella virus and, thus these nucleotide are very important. Among the above-mentioned 9 nucleotides, 4 nucleotides are found in gene 62 and 4 nucleotides are found in gene 71. Since gene 62 and gene 71 are contained in the inverted repeats (see Fig. 1), in the present invention, the quality control of an attenuated varicella live vaccine is conducted by subjecting the genomic DNA of a sample varicella vaccine virus to sequence analysis and confirming that the above-mentioned 1 nucleotide of gene 6 and 4 nucleotides of gene 62 are conserved without suffering mutation. For improving the exactness of the quality control, it is preferred that the sample virus is further confirmed to conserve the above-mentioned 4 nucleotides of gene 71 without suffering mutation.

[0016] Further in the present invention, it is preferred to confirm that the sample varicella vaccine virus conserves, without suffering mutation, all 58 nucleotides which are unique to the attenuated Oka strain. Specifically, together with the above-mentioned unique nucleotides of the attenuated Oka strain which show the XXY pattern and are nonsynonymous substitutions, the conservation of the following 49 nucleotides without suffering mutation is confirmed in the present invention:

the 560th C, the 703rd Y, the 763rd Y, the 2,515th Y, the 10,900th Y, the 12,779th Y, the 19,431st Y, the 26,125th G, the 31,732nd Y, the 38,036th Y, the 39,227th K, the 58,595th R, the 59,287th R, the 64,067th R, the 71,252nd Y, the 82,225th R, the 84,091st R, the 87,280th R, the 87,306th Y, the 89,734th R, the 90,535th R, the 94,167th C, the 97,748th R, the 97,796th Y, the 101,089th R, the 105,169th R, the 105,310th R, the 105,705th C, the 106,710th R, the 107,136th C, the 107,599th R, the 107,797th R, the 108,111st C, the 108,838th R, the 109,137th R, the 109,200th R, the 111,650th R, the 118,247th Y, the 120,697th Y, the 120,760th Y, the 121,059th Y, the 121,786th G, the 122,100th Y, the 122,298th Y, the 122,761st G, the 123,187th Y, the 124,192nd G, the 124,587th Y and the 124,728th Y,

wherein, R represents A or G, Y represents C or T, and K represents G or T.

[0017] In addition to the above-mentioned 58 nucleotide mutations, the following unique mutations of the attenuated Oka strain were found by the homology search conducted among the whole genomic DNA sequences of the Dumas strain, the parental Oka strain and the attenuated Oka strain: a deletion mutation in the origin of replication, a mutation in the repetitive region R1 of gene 11 and a mutation in the repetitive region R4 of the noncoding regions.

[0018] In a varicella virus genome, there are two origins of replication which are contained in the inverted repeats (see Fig. 1). The origins of replication are a region corresponding to the 110,087th to 110,350th nucleotides of the sense strand of the genomic DNA of the Dumas strain and a region corresponding to the 119,547th to 119,810th nucleotides of the antisense strand of the genomic DNA of the Dumas strain. The nucleotide sequence of the sense strand is shown in Table 4. As is apparent from Table 4, the deletion in the origins of replication of the attenuated Oka strain occur with

respect to segments each having a nucleotide sequence of TATATATATATA arranged in the direction of from the 5' end to the 3' end, and the segments are a segment corresponding to the 110,214th to 110,227th nucleotides of the sense strand and a segment corresponding to the 119,670th to 119,683rd nucleotides of the antisense strand. In the present invention, it is preferred that the presence of this deletion is further confirmed. Specifically, this deletion can be confirmed by determining the presence or absence of the segments each having a nucleotide sequence of ATATATATA which correspond to the 110,219th to 110,227th nucleotides of the sense strand and the 119,670th to 119,678th nucleotides of the antisense strand.

[0019] The repetitive region R1 of gene 11 is a region corresponding to the 13,937th to 14,242nd nucleotides of the genomic DNA of the Dumas strain, and the nucleotide sequence of the R1 region is shown in Table 5. As is apparent from Table 5, the nucleotide sequence of the R1 region of the attenuated Oka strain is different from that of not only the Dumas strain, but also the parental Oka strain. Therefore, for the quality control of the vaccine, it is preferred that the R1 region of the sample varicella vaccine virus is confirmed to be identical with the R1 region of the attenuated Oka strain. Specifically, it is confirmed that the repetitive sequence of one whole R1 region of the genomic DNA of the sample varicella vaccine virus is a nucleotide sequence of abbabba'bbb'abababx arranged in the direction of from the 5' end to the 3' end (wherein, a represents a nucleotide sequence of GGACGCGATCGACGACGA; a' represents a nucleotide sequence of GGACGCGATTGACGACGA; b represents a nucleotide sequence of GGGAGAGGCGGAGGA; b' represents a nucleotide sequence of GGACGCGGCGGAGGA; and x represents a nucleotide sequence of GGA).

[0020] In a varicella virus genome, two repetitive regions R4 which are contained in the inverted repeats are found in the noncoding regions (see Fig. 1). The R4 regions are a region corresponding to the 109,762nd to 109,907th nucleotides of the sense strand of the genomic DNA of the Dumas strain and a region corresponding to the 119,990th to 120,135th nucleotides of the antisense strand of the genomic DNA of the Dumas strain. The nucleotide sequence of the R4 region in the direction of the 5' end to the 3' end is shown in Table 7. As is apparent from Table 7, the repetitive sequence of the R4 region of the attenuated Oka strain is different from that of not only the Dumas strain, but also the parental Oka strain. Therefore, for the quality control of the vaccine, it is preferred that the R4 region of the sample varicella vaccine virus is confirmed to be identical with the R4 region of the attenuated Oka strain. Specifically, it is confirmed that the repetitive sequence of each of two whole R4 regions of the genomic DNA of the sample varicella vaccine virus is a nucleotide sequence of aaaaaaaaaaax arranged in the direction of from the 5' end to the 3' end (wherein, a represents a nucleotide sequence of CCCC GCCGATGGGGAGGGGGCGCGGTA; and x represents a nucleotide sequence of CCCC GCCGATG).

[0021] In addition, the mutations shown in Table 6 have been found in the repetitive region R3 of gene 22. However, as is apparent from Table 6, there is a large diversity among the repetitive sequences of the R3 region of the attenuated Oka strain and the parental Oka strain.

[0022] The method of the present invention has been completed based on the above-mentioned nucleotide mutations which are unique to the attenuated Oka strain. Therefore, the methods used in the methods for the quality control of the present invention can be used not only for the quality control of an attenuated varicella virus live vaccine (that is, determining whether a seed virus for a vaccine, an attenuated varicella virus as a raw material of a vaccine or a live vaccine has been mutated or not), but also for the identification of a virus strain capable of functioning as an attenuated varicella vaccine virus (a virus which can be used as an active ingredient of a varicella vaccine) and the analysis of a virulent strain (the parental Oka strain or a natural wild-type strain). In addition, the method of the present invention provides an exact and advantageous techniques to be used for tracing the effects of the vaccination and for the researches in the field of epidemiology of varicella and zoster, and also provides an exact measure for preventing varicella and zoster.

[0023] The specific methods for conducting the quality control of the present invention will be described in detail below.

[0024] Preparation of a genomic DNA of a sample varicella virus: In the method of the present invention, a virus suspension or a bulk vaccine solution for use as an active ingredient of an attenuated varicella live vaccine, a virus suspension obtained by propagating a desired VZV, and vesicle fluid and the like obtained from a naturally infected varicella patient can be used as a sample varicella virus. The genomic DNA can be extracted and purified directly from the sample viruses by a conventional method. Alternatively, cells can be infected with VZV to be used as the sample virus, and the genomic DNA of the virus can be extracted and purified from the infected cells by a conventional method (with respect to the methods for extracting and purifying a DNA, reference can be made to "Current Protocol in Molecular Biology", Volume 1, Chapter 2, 2.0.1-2.6.12, John Wiley & Sons, Inc., 1987-2000 (the loose-leaf system)). For propagating the VZV, WI-38 cells and MRC-5 cells can be used. It is preferred that the vesicle fluid used as a material for isolating, propagating and preparing a fresh wild-type strain or an epidemic strain is obtained from a naturally infected patient within 3 days after the onset of varicella.

[0025] Preparation of PCR primers: A desired nucleotide sequence of a VZV genomic DNA can be amplified by a PCR method. First, polynucleotide strands consisting of contiguous sequences of about 15 to 30 nucleotides which correspond to the 5'-terminal sequence of the sense and antisense sequences of the desired region are prepared by a DNA synthesizer. The prepared polynucleotide strands are used as a pair of primers. The whole genomic DNA sequence of the attenuated Oka strain shown in SEQ ID NO:2 and the patent documents mentioned under "Prior Art" of the

specification (U.S. Patent No. 6,093,535 and International Application Publication WO 00/50603) can be referred when designing the PCR primers.

[0026] Determination of the nucleotide sequence of the PCR products: From the view point of saving labor for conducting the experiments, it is preferred that the PCR products are analyzed by a direct DNA sequencing method without the preparation of a genomic DNA library (this method is described in "Current Protocol in Molecular Biology", Volume 3, Chapter 15, 15.2.1-15.2.11, ditto). In this method, the sequencing of a nucleotide sequence can be determined by conventional methods, for example, dideoxy method, a method using Cycle Sequence Kit (manufactured and sold by TAKARA SHUZO Co. Ltd., Japan), and a method using DNA Sequencing Kit (manufactured and sold by Perkin Elmer Applied Biosystems, USA).

[0027] Homology search of DNA sequences: Homology search of DNA sequences can be performed using commercially available computer software for gene analysis. For example, GENETYX-WIN (ver. 3.1) (manufactured and sold by Software Development Co., Ltd., Japan), DNASIS (ver. 3.7) (manufactured and sold by Hitachi Software Engineering Co., Ltd., Japan), FASTA (<http://www.ddjb.nig.ac.jp/>), and BLAST (<http://www.ncbi.nlm.nih.gov/>) can be used. Whether or not a sample varicella vaccine virus has a specific nucleotide sequence of the attenuated varicella Oka strain disclosed in the present specification can be determined by a homology search.

[0028] Confirmation of a nucleotide mutation by an RFLP analysis: In addition to the homology search conducted after determining the (whole or partial) nucleotide sequence of the genomic DNA of a sample virus, an RFLP (Restriction Fragment Length Polymorphism) analysis can be conducted to confirm that the unique nucleotides of the attenuated Oka strain are conserved by the sample virus without suffering mutation. Specifically, polynucleotide strands consisting of contiguous sequences of about 15 to 30 nucleotides which correspond to the 5'-terminal sequence of the sense and antisense sequences of the desired region are prepared by a DNA synthesizer, and the prepared polynucleotide strands are used as a pair of PCR primers. A pair of PCR primers are simultaneously used for amplifying the desired region to be used as a sample DNA. Thus obtained sample DNA is digested with a restriction enzyme and applied to a gel electrophoresis. The presence of a mutation can be determined by the difference in the size of the detected DNA fragments. The RFLP analysis which is easier to perform than the homology search is preferably used in the method for the quality control of the present invention. With respect to the 9 specific nucleotide mutations of the attenuated Oka strain which show the XXY pattern and are nonsynonymous substitutions (the 5,745th G, the 105,356th C, the 105,544th G, the 106,262nd C, the 107,252nd C, the 122,645th G, the 123,635th G, the 124,353rd C and the 124,541st G), and the 560th C, the 26,125th G, the 94,167th C, the 105,705th C, the 107,136th C, the 108,111st C, the 121,786th G, the 122,761st G and the 124,192nd G among the remaining 49 nucleotide mutations of the attenuated Oka strain, the presence or the absence of the mutations can be determined by the RFLP analysis using the eight primer pairs shown in Table 8 (SEQ ID NOs: 3 to 18). The restriction sites of the PCR products obtained by using the PCR primers shown in Table 8 are summarized in Table 9, together with the sizes of the restriction fragments. For example, the mutation of gene 6 (the 5,745th nucleotide G found in gene 6 of the attenuated Oka strain) can be detected by the absence or presence of the restriction enzyme Alu I site. Specifically, 763 bp DNA fragment corresponding to the 5,372nd to 6,134th nucleotides of the genomic DNA of a sample varicella vaccine virus is amplified using the primers 01-N12 and 01-R13 shown in Table 8. The amplified fragment is digested with Alu I and applied to an agarose gel electrophoresis. In the case of a virulent strain, the PCR product is cleaved into three fragments (170 bp, 205 bp and 388 bp). On the other hand, the PCR product of the attenuated Oka strain is cleaved into two fragments (170 bp and 593 bp). Therefore, whether or not a sample varicella vaccine virus is a virus capable of functioning as a vaccine strain can be determined from the restriction-fragment pattern.

[0029] In the present invention, the 9 unique nucleotide mutations of the attenuated Oka strain which show the XXY pattern and are nonsynonymous substitutions are preferably confirmed by the RFLP analysis using the following primers: a pair of primers of SEQ ID NOs: 5 and 6 with respect to the confirmation of the 5,745th G; a pair of primers of SEQ ID NOs: 11 and 12 with respect to the confirmation of the 105,356th C, the 105,544th G, the 124,353rd C and the 124,541st G; a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 106,262nd C and the 123,635th G; and a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 107,252nd C and the 122,645th G. Since gene 62 and gene 71 are inverted repeats (see Fig. 1), the quality control of an attenuated varicella live vaccine can be conducted by confirming the conservation of at least 5 nucleotides (namely 1 nucleotide of gene 6 and 4 nucleotides of gene 62) by the RFLP analysis.

[0030] As mentioned above, the whole genomic DNA sequence of the attenuated Oka strain (SEQ ID NO:2) and the nucleotide mutations which are unique to the attenuated Oka strain have been disclosed for the first time by the present inventors. Since the unique nucleotide mutations of the attenuated Oka strain are considered to be very important for the attenuation of a varicella viruses, an attenuated strain can be constructed by introducing a nucleotide substitution to a genomic DNA of a virulent strain (for example a wild type VZV strain or an epidemic strain), or by inducing an amino acid mutation in a virulent strain. The method described in Proc. Natl. Acad. Sci., USA, 90(15), 7376-7380, 1998 can be used as a genetic engineering technique for inducing a nucleotide or amino acid mutation. Specifically, the 58 nucleotide mutations which are unique to the attenuated Oka strain can be used as an index for inducing a mutation to

a virulent strain, and the 9 nucleotide substitutions which are nonsynonymous substitutions are especially useful. In addition, taking into account the fact that gene 62 and gene 71 are contained in the inverted repeats (see Fig. 1), among the above-mentioned nucleotide substitutions, at least 5 nucleotide mutations (namely a mutation found in gene 6 and the mutations found in either gene 62 or gene 71) are considered to be very important.

BEST MODE FOR CARRYING OUT THE INVENTION

[0031] Hereinbelow, the present invention will be described in more detail with reference to the following Examples, but they should not be construed as limiting the scope of the present invention.

Example 1

[0032] The attenuated Oka strain (attenuated vaccine strain) and its parental strain (parental Oka strain; a virulent strain which is not attenuated) were individually inoculated into MRC-5 cells to thereby obtain infected cells. The genomic DNAs of the attenuated Oka strain and the parental Oka strain were extracted individually from the infected cells by phenol extraction and chloroform/isoamyl alcohol extraction, and purified by ethanol precipitation, thereby obtaining DNA. PCR products covering the entire genome of each strain were prepared using the obtained DNA as a template and 88 synthetic primers (44 primer pairs). Subsequently, the nucleotide sequences of the PCR products were determined by the direct DNA sequencing method using 520 synthetic primers and the DNA Sequencing Kit (manufactured and sold by Perkin Elmer Applied Biosystems, USA). Using the whole genomic sequence of the Dumas strain (virulent strain) shown in SEQ ID NO: 1 as a standard, the homology search was conducted with respect to the obtained whole genomic DNA sequences of the attenuated Oka strain and the parental Oka strain. DNASIS (version 3.7) (manufactured and sold by Hitachi Software Engineering Co., Ltd., Japan) was used for conducting the homology search. The characteristics of the attenuated Oka strain which became apparent from the homology search are summarized in Tables 1 to 7.

[0033] The nucleotide mutations which were detected by comparing the sequences among the three varicella strains (Dumas strain, parental Oka strain and attenuated Oka strain) are listed in Table 1. Specifically, the nucleotide number, the gene number, the mutated nucleotide and the amino acid mutation caused by the nucleotide mutation are described for each nucleotide mutation. In Table 1, Y represents a pyrimidine base (i.e., C or T), R represents a purine base (i.e., A or G), K represents G or T, (ncr) represents a noncoding region, an alphabet letter in parentheses (for example "(W)") is a one-letter abbreviation of an amino acid, (och) represents ochre codon, (amb) represents amber codon, (W/R) represents tryptophan (W) or arginine (R), and (del) represents deletion.

[0034] Among the mutations listed in Table 1, the mutations which were detected by the sequence alignment between the attenuated Oka strain and the parental Oka strain are listed in Table 2. Specifically, the nucleotide number, the gene number, the mutated nucleotide and the amino acid mutation caused by the nucleotide mutation are described for each nucleotide mutation. In Table 2, X/Y represents X or Y, and a three-letter abbreviation of an amino acid encoded by a nucleotide is shown in parentheses following the nucleotide (when a nucleotide is located in a noncoding region, the nucleotide is followed by "(ncr)"). All other abbreviations used in Table 2 are the same as those used in Table 1.

[0035] The nucleotide mutations described in Tables 1 and 2 are summarized in Table 3, based on the mutation patterns. The mutation patterns and abundance thereof are listed together with the details of the mutation patterns, that is, the specific types of mutation (a stop codon (och/amb) mutation, a synonymous or nonsynonymous substitution, and deletion (or addition)) and the abundance of each type of mutation.

[0036] The findings based on Tables 1 to 3 are explained in detail below.

[0037] Among the major nucleotide and amino acid mutations which were determined by the comparison between the whole genomic DNA sequences of the attenuated Oka strain and the parental Oka strain, the mutations described in the following items (a) to (f) were found to be especially useful and important for the quality control of an attenuated varicella live vaccine.

(a) There were 58 important nucleotide mutations of the attenuated Oka strain, namely 18 nucleotide mutations showing the XXY pattern and 40 nucleotide mutations showing the XX(X/Y) pattern.

(b) Among the above-mentioned 58 mutations, 49 mutations were found in the coding regions, 8 mutations were found in the noncoding regions and 1 mutation was found in a stop codon.

(c) Among the 49 mutations found in the coding regions, 29 mutations were nonsynonymous substitutions and 20 mutations were synonymous substitutions.

(d) Among the 18 mutations showing the XXY pattern, 9 mutations were nonsynonymous substitutions, 8 mutations were synonymous substitutions, and 1 mutation was found in a noncoding region.

(e) The above-mentioned 9 mutations showing the XXY pattern which are nonsynonymous substitutions (namely the 5,745th nucleotide G of gene 6; the 105,356th nucleotide C, the 105,544th nucleotide G, the 106,262nd nucleotide C and the 107,252nd nucleotide C of gene 62; and the 122,645th nucleotide G, the 123,635th nucleotide G, the

124,353rd nucleotide C and the 124,541st nucleotide G of gene 71) can be used as markers for the attenuation or safety of a virus strain capable of functioning as an active ingredient of a live vaccine. Therefore, these nucleotide mutations are useful and important for the quality control of a vaccine. It should be noted that gene 62 and gene 71 are contained in the inverted repeats (see Fig. 1).

(f) 40 nucleotides of the vaccine strain showed the XX(X/Y) pattern (that is, a mutation pattern wherein the virus strain is a mixture of a virus having nucleotide X and a virus having nucleotide Y). When the attenuated Oka strain was subcultured experimentally (i.e., the virus was passaged 5 times, 10 times, 17 times and the like), all the nucleotides of the XX(X/Y) pattern, except for the 106,710th nucleotide, showed the following tendency. The detection frequency of nucleotide Y increased in accordance with the number of passages (that is, the nucleotide changed from X/Y to Y) and the mutation pattern of the nucleotide converged to the XXY pattern. In other words, the ratio of X to Y (x/y) decreased in accordance with the number of passages. Based on the above-mentioned phenomenon, it is considered that the number of passages of a seed virus used in a seed lot system can be estimated by measuring the x/y value. It should be noted that among the above-mentioned mutations, 20 mutations converged to nonsynonymous substitutions. With respect to the remainder of the mutations, 12 mutations were synonymous substitutions, 1 mutation was found in a stop codon (specifically, an ochre codon/amber codon mixture converged to an amber mutation), and 7 mutations were found in the noncoding regions.

Table 1

Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
1	5'/gene 1	A (ncr)	G (ncr)	G (ncr)
3	5'/gene 1	G (ncr)	C (ncr)	C (ncr)
117	5'/gene 1	C (ncr)	del	del
236	5'/gene 1	A (ncr)	G (ncr)	G (ncr)
262	5'/gene 1	C (ncr)	T (ncr)	T (ncr)
560	5'/gene 1	T (ncr)	T (ncr)	C (ncr)
685	gene 1	G (N)	A (N)	A (N)
703	gene 1	T (Q)	T (Q)	Y (Q)
763	gene 1	T (P)	T (P)	Y (P)
789	gene 1	T (T)	C (A)	C (A)
790-1	gene 1	TT (Q)	CC (R)	CC (R)
2515	gene 3/4	T (ncr)	T (ncr)	Y (ncr)
3764	gene 4	A (T)	G (T)	G (T)
4258	gene 5	C (K)	T (K)	T (K)
5745	gene 6	A (S)	A (S)	G (P)
6853	gene 6	G (H)	T (Q)	T (Q)
7091	gene 6	C (G)	A (V)	A (V)
7753	gene 6	C (P)	T (P)	T (P)
9460	gene 7/8	T (ncr)	C (ncr)	C (ncr)
10079	gene 8	G (P)	A (S)	A (S)
10900	gene 9A	T (W)	T (W)	Y (W/R)
11890	gene 9	T (S)	G (S)	G (S)
11906	gene 9	A (T)	G (A)	G (A)
12188	gene 10	C (P)	A (H)	A (H)
12284	gene 10	T (F)	C (S)	C (S)
12285	gene 10	T (F)	C (S)	C (S)
12779	gene 10	C (A)	C (A)	Y (A/V)
13173	gene 10	T (G)	G (G)	G (G)
13407	gene 10/11	G (ncr)	A (ncr)	A (ncr)
14390	gene 11	T (C)	C (C)	C (C)
17404	gene 12	C (V)	T (V)	T (V)

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
5	17834	gene 12	C (L)	T (L)	T (L)
	18082	gene 12	C (T)	T (T)	T (T)
	18467	gene 13	G (K)	A (K)	A (K)
	19431	gene 14	T (o)	T (o)	Y (o/a)
10	19719	gene 14	A (I)	G (I)	G (I)
	20656	gene 14	T (Y)	A (F)	A (F)
	20684	gene 14	T (T)	C (A)	C (A)
	21371	gene 15	G (L)	A (L)	A (L)
15	21734	gene 15	G (R)	T (R)	T (R)
	22311	gene 15	G (S)	A (S)	A (S)
	22504	gene 15/16	A (ncr)	G (ncr)	G (ncr)
	22794	gene 16	A (M)	G (T)	G (T)
20	23294	gene 16	A (F)	G (F)	G (F)
	24515-7	gene 17	TCA (S)	del	del
	24578	gene 17	A (T)	G (A)	G (A)
	24654	gene 17	C (T)	T (M)	T (M)
25	25067	gene 17	G (V)	A (I)	A (I)
	26125	gene 18	A (N)	A (N)	G (N)
	27523	gene 19	A (H)	G (H)	G (H)
	29201	gene 20	T (G)	G (G)	G (G)
30	31732	gene 21	C (T)	C (T)	Y (T/I)
	32274	gene 21	A (T)	G (A)	G (A)
	33722	gene 21	T (H)	C (H)	C (H)
	33725	gene 21	T (D)	C (D)	C (D)
35	33728	gene 21	T (N)	C (N)	C (N)
	35543	gene 22	T (V)	C (V)	C (V)
	37649	gene 22	A (L)	G (L)	G (L)
	37902	gene 22	A (I)	G (V)	G (V)
40	38036	gene 22	T (T)	T (T)	Y (T)
	38055	gene 22	T (V)	C (H)	C (H)
	38081	gene 22	A (P)	C (P)	C (P)
	38177	gene 22	G (E)	A (E)	A (E)
45	38714	gene 22	G (T)	T (T)	T (T)
	38717	gene 22	C (A)	T (A)	T (A)
	39023	gene 22	A (R)	G (R)	G (R)
	39227	gene 22	T (P)	T (P)	K (P)
50	39263	gene 22	G (Q)	A (Q)	A (Q)
	39394	gene 22	G (R)	A (H)	A (H)
	39530	gene 22	A (V)	G (V)	G (V)
	40388	gene 22	A (Q)	G (Q)	G (Q)
55	41057	gene 22	T (P)	C (P)	C (P)
	41452	gene 22	G (R)	A (Q)	A (Q)
	41618	gene 22	C (T)	T (T)	T (T)
	41764	gene 22	G (S)	A (N)	A (N)
55	42069	gene 22	C (Q)	G (E)	G (E)
	42176	gene 22	C (R)	T (R)	T (R)
	42242	gene 22	A (A)	C (A)	C (A)
	42401-3	gene 22/23	AAA (ncr)	del	del

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
5	42476	gene 23	T (S)	G (S)	G (S)
	43262	gene 24	T (I)	C (V)	C (V)
	44835	gene 26	C (C)	T (C)	T (C)
	47162	gene 28	A (C)	G (R)	G (R)
	47940	gene 28	C (L)	T (L)	T (L)
10	48050	gene 28	T (S)	C (G)	C (G)
	48825	gene 28	G (T)	A (T)	A (T)
	49535	gene 28	G (L)	A (L)	A (L)
	50081	gene 28	C (G)	A (C)	A (C)
	51168	gene 29	C (S)	T (S)	T (S)
15	52917	gene 29	A (Q)	G (Q)	G (Q)
	53482	gene 29	A (I)	C (L)	C (L)
	53938	gene 29	G (A)	A (T)	A (T)
	54359-73	gene 29	AACTTTC GGGTCA (NISGS)	del	del
	54562	gene 29/30	T (ncr)	del (ncr)	del (ncr)
20	54564	gene 29/30	T (ncr)	C (ncr)	C (ncr)
	55820	gene 30	A (P)	G (P)	G (P)
	57224	gene 31	A (T)	C (P)	C (P)
	57301	gene 31	A (A)	C (A)	C (A)
	57397	gene 31	G (A)	T (A)	T (A)
25	58595	gene 31	A (I)	A (I)	R (I/V)
	59287	gene 31	A (P)	A (P)	R (P)
30	59760-1	gene 31/32	del (ncr)	G (ncr)	G (ncr)
	60276-8	gene 32/33	AAA (ncr)	del	del
	60279	gene 32/33	A (ncr)	C (ncr)	C (ncr)
	60405	gene 33	C (A)	A (A)	A (A)
	60781	gene 33	T (Y)	G (S)	G (S)
35	61018-9	gene 33	GG (P)	AA (F)	AA (F)
	61201-2	gene 33	TT (N)	CC (G)	CC (G)
	64067	gene 35	A (A)	A (A)	R (A)
	64136	gene 35	A (C)	G (C)	G (C)
	64259	gene 35	T (P)	C (P)	C (P)
40	64375	gene 35	T (M)	C (V)	C (V)
	64989	gene 36	C (A)	T (A)	T (A)
	65669	gene 36	C (S)	T (L)	T (L)
	66646	gene 37	G (L)	T (L)	T (L)
	66879	gene 37	C (P)	T (L)	T (L)
45	68172	gene 37	G (R)	A (K)	A (K)
	69349	gene 38	A (T)	G (T)	G (T)
	69756	gene 38	T (S)	C (G)	C (G)
	71252	gene 39	T (M)	T (M)	Y (M/T)
50	72997	gene 40	C (V)	T (V)	T (V)
	73993	gene 40	T (T)	C (T)	C (T)
	76530	gene 41	C (V)	T (V)	T (V)
	78144	gene 42/43	T (ncr)	del	del
	80244	gene 43/44	G (ncr)	T (ncr)	T (ncr)
55	80840	gene 44	A (N)	G (D)	G (D)
	81187	gene 44	C (A)	T (A)	T (A)

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
	82225	gene 45	A (P)	A (P)	R (P)
5	84091	gene 47	G (E)	G (E)	R (E)
	84616	gene 47	A (T)	G (T)	G (T)
	84983	gene 48	G (R)	A (H)	A (H)
	85563	gene 48	C (D)	T (D)	T (D)
10	86170	gene 48	C (Q)	A (K)	A (K)
	86484-93	gene 49/50	CCTGATAA AC (ncr)	del (ncr)	del (ncr)
	86556	gene 49/50	T (ncr)	G (ncr)	G (ncr)
	87280	gene 50	A (C)	A (C)	R (C)
15	87306	gene 50	T (S)	T (S)	Y (S/G)
	87841	gene 50	C (S)	T (S)	T (S)
	88477	gene 51	G (S)	T (S)	T (S)
	89734	gene 51	A (T)	A (T)	R (T)
20	89905	gene 51	T (T)	C (T)	C (T)
	90202	gene 51	G (Q)	T (H)	T (H)
	90217	gene 51	T (S)	C (S)	C (S)
	90392	gene 51/52	G (ncr)	A (ncr)	A (ncr)
	90535	gene 52	A (I)	A (I)	R (I/V)
25	91191	gene 52	C (G)	T (G)	T (G)
	92026	gene 52	(T)	G (A)	G (A)
	92092	gene 52	(T)	G (A)	G (A)
	92375	gene 52	(H)	G (R)	G (R)
30	92999	gene 53	(V)	C (V)	C (V)
	94167	gene 54	T (L)	T (L)	C (L)
	94632	gene 54	A (V)	G (V)	G (V)
	94641	gene 54	A (T)	T (T)	T (T)
35	95241	gene 54	T (G)	C (G)	C (G)
	95546	gene 54	G (L)	A (L)	A (L)
	95601	gene 54	T (E)	G (D)	G (D)
	97141	gene 55	T (L)	C (L)	C (L)
	97591	gene 55	C (I)	T (I)	T (I)
40	97748	gene 55	G (A)	G (A)	R (A/T)
	97796	gene 55	T (C)	T (C)	Y (C/R)
	98437	gene 55	T (G)	C (G)	C (G)
	98765	gene 56	A (V)	C (V)	C (V)
45	98807	gene 56	A (T)	C (T)	C (T)
	99226-8	gene 56	CTT (S)	del	del
	99421	gene 57	T (H)	G (P)	G (P)
	99709	gene 57	A (Y)	G (Y)	G (Y)
50	99981	gene 58	C (V)	T (K)	T (K)
	100114	gene 58	T (K)	A (N)	A (N)
	100151	gene 58	T (N)	G (T)	G (T)
	100283	gene 58/59	A (ncr)	G (ncr)	G (ncr)
	101089	gene 59	A (L)	A (L)	R (L/P)
55	101331	gene 60	C (A)	T (T)	T (T)
	101623-4	gene 60	del	ATC (H)	ATC (H)
	101886	gene 60/61	T (ncr)	C (ncr)	C (ncr)

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
5	101991	gene 60/61	C(ncr)	T (ncr)	T (ncr)
	102192	gene 60/61	G (ncr)	A (ncr)	A (ncr)
	102203	gene 60/61	A (ncr)	G (ncr)	G (ncr)
	102309	gene 60/61	C (ncr)	A (ncr)	A (ncr)
	102351	gene 60/61	A (ncr)	C (ncr)	C (ncr)
10	102458	gene 60/61	A (ncr)	G (ncr)	G (ncr)
	102601	gene 60/61	T (ncr)	G (ncr)	G(ncr)
	103043	gene 60/61	T (ncr)	C (ncr)	C(ncr)
	104898	gene 61/62	A (ncr)	G (ncr)	G (ncr)
	105009-10	gene 61/62	del	G(ncr)	G(ncr)
15	105012	gene 61/62	T (ncr)	C (ncr)	C (ncr)
	105015	gene 61/62	T (ncr)	C (ncr)	C (ncr)
	105017	gene 61/62	T (ncr)	C (ncr)	C (ncr)
	105054	gene 61/62	G (ncr)	del	del
	105071	gene 61/62	G (ncr)	del	del
20	105151-2	gene 61/62	del (ncr)	ACAA (ncr)	ACAA (ncr)
	105169	gene 61/62	A (ncr)	A (ncr)	R (ncr)
25	105310	gene 62	A (L)	A (L)	R (L/S)
	105312	gene 62	A (G)	G (G)	G (G)
	105356	gene 62	T (I)	T (I)	C (V)
	105451	gene 62	A (L)	G (P)	G (P)
	105512	gene 62	A (S)	C (A)	C (A)
30	105544	gene 62	A (V)	A (V)	G (A)
	105705	gene 62	T (A)	T (A)	C (A)
	106262	gene 62	T (R)	T (R)	C (G)
	106710	gene 62	A (A)	A (A)	R (A)
	107136	gene 62	T (A)	T (A)	C (A)
35	107165	gene 62	C (A)	T (T)	T (T)
	107252	gene 62	T (S)	T (S)	C (G)
	107307	gene 62	T (R)	C (R)	C (R)
40	107599	gene 62	A (V)	A (V)	R (V/A)
	107607	gene 62	C (T)	A (T)	A (T)
	107715	gene 62	T (A)	C (A)	C (A)
	107797	gene 62	A (L)	A (L)	R (L/P)
45	108111	gene 62	T (P)	T (P)	C (P)
	108747	gene 62	A (L)	G (L)	G (L)
	108838	gene 62	A (M)	A(M)	R(M/T)
50	108951	gene 62	G (H)	A (M)	A (M/T)
	109044	gene 62	C (A)	G(A)	G(A)
	109137	gene 62/63	A (ncr)	A (ncr)	R (ncr)
	109200	gene 62/63	A (ncr)	A (ncr)	R (ncr)
55	109654	gene 62/63	G (ncr)	T (ncr)	T (ncr)
	109696-7	gene 62/63	del	CAT (ncr)	CAT (ncr)
	110003	gene 62/63	G (ncr)	A(ncr)	A(ncr)
	110058	gene 62/63	G (ncr)	del	del

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
5	110112	gene 62/63	G (ncr)	A(ncr)	A (ncr)
	110378	gene 62/63	G (ncr)	del	del
	110386	gene 62/63	C (ncr)	del	del
	111312	gene 63	A (T)	G(T)	G(T)
	111650	gene 64	A (Q)	A (Q)	R (Q/R)
10	112093	gene 64	T (Y)	C (H)	C (H)
	112137	gene 64/65	A (ncr)	del	del
	112198	gene 64/65	G (ncr)	A(ncr)	A (ncr)
	114140	gene 66	A (S)	G (S)	G (S)
	115041	gene 67	G (P)	A (P)	A (P)
15	115926	gene 68	C (T)	T (I)	T (I)
	117699	gene 68/69	C (ncr)	T (ncr)	T (ncr)
	117760	gene 68/69	T (ncr)	del	del
	117804	gene 69	A (Y)	G (H)	G (H)
	118247	gene 69	T (Q)	T (Q)	Y (Q/R)
20	118585	gene 70	T (T)	C (T)	C (T)
	119511	gene 70/71	G (ncr)	del	del
	119519	gene 70/71	C (ncr)	del	del
	119785	gene 70/71	C (ncr)	T (ncr)	T (ncr)
	119839	gene 70/71	C (ncr)	del	del
25	119894	gene 70/71	C (ncr)	T (ncr)	T (ncr)
	120200-1	gene 70/71	del	ATG (ncr)	ATG (ncr)
	120243	gene 70/71	C (ncr)	A (ncr)	A (ncr)
	120697	gene 70/71	T (ncr)	T (ncr)	Y (ncr)
	120760	gene 70/71	T (ncr)	T (ncr)	Y (ncr)
30	120853	gene 71	G (A)	C (A)	C (A)
	120946	gene 71	C (H)	T(H)	T(H)
	121059	gene 71	T (M)	T (M)	Y(M/T)
	121150	gene 71	T (L)	C (L)	C (L)
	121786	gene 71	A (P\$)	A(P)	G(P)
35	122100	gene 71	T (L)	T (L)	Y (L/P)
	122182	gene 71	A (A)	G (A)	G (A)
	122290	gene 71	G (T)	T(T)	T(T)
	122298	gene 71	T (V)	T(V)	Y(V/A)
	122590	gene 71	A (R)	G (R)	G (R)
40	122645	gene 71	A (S)	A (S)	G (G)
	122732	gene 71	G (A)	A (T)	A (T)
	122761	gene 71	A (A)	A (A)	G (A)
	123187	gene 71	T (A)	T (A)	Y (A)
	123635	gene 71	A (R)	A (R)	G (G)
45	124192	gene 71	A (A)	A (A)	G (A)
	124353	gene 71	T (V)	T (V)	C (A)
	124385	gene 71	T (S)	G (A)	G (A)
	124446	gene 71	T (L)	C (P)	C (P)
	124541	gene 71	A (I)	A (I)	G (V)

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(continued)

	Nucleotide no.	Gene no.	Dumas strain	Parental Oka strain	Attenuated Oka strain
5	124585	gene 71	T (G)	C (G)	C (G)
	124587	gene 71	T (L)	T (L)	Y (L/S)
	124728	gene 71/3'	T (ncr)	T (ncr)	Y (ncr)
	124745-6	gene 71/3'	del (ncr)	TTGT (ncr)	TTGT (ncr)
10	124826	gene 71/3'	C (ncr)	del	del
	124843	gene 71/3'	C (ncr)	del	del
	124880	gene 71/3'	A (ncr)	G (ncr)	G (ncr)
	124882	gene 71/3'	A (ncr)	G (ncr)	G (ncr)

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Table 2

	Gene no.	Nucleotide no.	Attenuated Oka strain	Parental Oka strain	Dumas strain
20	1	560	C (ncr)	T (ncr)	T (ncr)
		703	T/C (Gln)	T (Gln)	T (Gln)
		763	T/C (Pro)	T (Pro)	T (Pro)
25	3-4	2515	T/C (ncr)	T (ncr)	T (ncr)
	6	5745	G (Pro)	A (Ser)	A (Ser)
	9A	10900	T/C (Trp/Arg)	T (Trp)	T (Trp)
	10	12779	C/T (Ala/Val)	C (Ala)	C (Ala)
	14	19431	T/C (och/amb)	T (och)	T (och)
	18	26125	G (Asn)	A (Asn)	A (Asn)
	21	31732	C/T (Thr/Ile)	C (Thr)	C (Thr)
30	22	38036	T/C (Thr)	T (Thr)	T (Thr)
		39227	G/T (Pro)	T (Pro)	T (Pro)
35	31	58595	A/G (Ile/Val)	A (Ile)	A (Ile)
		59287	A/G (Pro)	A (Pro)	A (Pro)
40	35	64067	A/G (Ala)	A (Ala)	A (Ala)
	39	71252	T/C (Met/Thr)	T (Met)	T (Met)
	45	82225	A/G (Pro)	A (Pro)	A (Pro)
	47	84091	A/G (Glu)	G (Glu)	G (Glu)
	50	87280	A/G (Cys)	A (Cys)	A (Cys)
45	50	87306	T/C (Ser/Gly)	T (Ser)	T (Ser)
50	51	89734	A/G (Thr)	A (Thr)	A (Thr)
	52	90535	A/G (Ile/Val)	A (Ile)	A (Ile)
	54	94167	C (Leu)	T (Leu)	T (Leu)
	55	97748	G/A (Ala/Thr)	G (Ala)	G (Ala)
55	59	97796	T/C (Cys/Arg)	T (Cys)	T (Cys)
55	59	101089	A/G (Leu/Pro)	A (Leu)	A (Leu)
	61-62	105169	A/G (ncr)	A (ncr)	A (ncr)

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(continued)

	Gene no.	Nucleotide no.	Attenuated Oka strain	Parental Oka strain	Dumas strain
5	62	105310	A/G (Leu/Ser)	A (Leu)	A (Leu)
		105356	C (Val)	T (Ile)	T (Ile)
		105544	G (Ala)	A (Val)	A (Val)
		105705	C (Ala)	T (Ala)	T (Ala)
		106262	C (Gly)	T (Arg)	T (Arg)
10		106710	A/G (Ala)	A (Ala)	A (Ala)
		107136	C (Ala)	T (Ala)	T (Ala)
		107252	C (Gly)	T (Ser)	T (Ser)
		107599	A/G (Val/Ala)	A (Val)	A (Val)
		107797	A/G (Leu/Pro)	A (Leu)	A (Leu)
15		108111	C (Pro)	T (Pro)	T (Pro)
		108838	A/G (Met/Thr)	A (Met)	A (Met)
	62-63	109137	A/G (ncr)	A (ncr)	A (ncr)
20		109200	A/G (ncr)	A (ncr)	A (ncr)
	64	111650	A/G (Gln/Arg)	A (Gln)	A (Gln)
	69	118247	T/C (Gln/Arg)	T (Gln)	T (Gln)
25					
	70-71	120697	T/C (nrc)	T (nrc)	T (nrc)
		120760	T/C (nrc)	T (nrc)	T (nrc)
	71	121059	T/C (Met/Thr)	T (Met)	T (Met)
30		121786	G (Pro)	A (Pro)	A (Pro)
		122100	T/C (Leu/Pro)	T (Leu)	T (Leu)
		122298	T/C (Val/Ala)	T (Val)	T (Val)
		122645	G (Gly)	A (Ser)	A (Ser)
35		122761	G (Ala)	A (Ala)	A (Ala)
		123187	T/C (Ala)	T (Ala)	T (Ala)
		123635	G (Gly)	A (Arg)	A (Arg)
		124192	G (Ala)	A (Ala)	A (Ala)
		124353	C (Ala)	T (Val)	T (Val)
40		124541	G (Val)	A (Ile)	A (Ile)
		124587	T/C (Leu/Ser)	T (Leu)	T (Leu)
	71-3'	124728	T/C (ncr)	T (ncr)	T (ncr)
45	ncr: noncoding region X/Y: X or Y och/amb: stop codon mutation of an ochre codon or an amber codon				

Table 3

	Pattern of nucleotide mutation	Dumas strain	Parental Oka strain	Attenuated Oka strain	Amino acid replacement	Number of nucleotides
55	XXX pattern	○	○	○		124,585

(continued)

	Pattern of nucleotide mutation	Dumas strain	Parental Oka strain	Attenuated Oka strain	Amino acid replacement	Number of nucleotides
5						189
	XYX pattern	○	●	●	Synonymous Nonsynonymous ncr	91 62 36
10						18
	XXY pattern	○	○	●	Synonymous Nonsynonymous ncr	8 9 1
15						40
	XX(X/Y) pattern	○	○	○/●	Synonymous Nonsynonymous ncr och/amb	12 20 7 1
20	XYX pattern	○	●	○		0
	XYZ pattern	○	●	◆		0
25	XDD pattern	○	del	del		52
	DXX pattern	del	○	○		19

XXX pattern: All three strains have the same nucleotide at a nucleotide number which corresponds to the same nucleotide site (i.e. "corresponding nucleotide number").

XYX pattern: Only the Dumas strain has a different nucleotide at the corresponding nucleotide number.

XXY pattern: Only the attenuated Oka strain has a different nucleotide at the corresponding nucleotide number.

XX(X/Y) pattern: Only the attenuated Oka strain has a nucleotide X/Y (X or Y) at the corresponding nucleotide number.

Therefore, the attenuated Oka strain is a mixture of the XXX and XXY patterns. For example, with respect to the 8 mutations showing the XX(X/Y) pattern which are located in gene 62, the ratio of x to y (x/y) transiently decreased as the number of passages increased from 5 times, 10 times to 17 times, and the mutation pattern converged to the XXY pattern. However, only the 106,710th nucleotide A/G remained unchanged without converging from A to G.

XYX pattern: Only the parental Oka strain has a different nucleotide at the corresponding nucleotide number.

XYZ pattern: All three strains have a different nucleotide at the corresponding nucleotide number.

XDD pattern: The nucleotide at the corresponding nucleotide number is either deleted (del) in both the parental Oka strain and the attenuated Oka strain, or added in only the Dumas strain.

DXX pattern: The nucleotide at the corresponding nucleotide number is either deleted (del) in only the Dumas strain, or added in both the parental Oka strain and the attenuated Oka strain.

ncr: noncoding region

och/amb: stop codon mutation of an ochre codon or an amber codon

[0038] Table 4 shows the sequence alignment of the nucleotide sequences of the sense strand of the origin of replication of the Dumas strain, the parental Oka strain and the attenuated Oka strain. In this table, "-" represents a deletion.

[0039] In the attenuated Oka strain, deletions occur with respect to segments each having a nucleotide sequence of TATATATATATATA arranged in the direction of from the 5' end to the 3' end, which correspond to the 110,214th to 110,227th nucleotides of the sense strand of the genomic DNA of the Dumas strain of SEQ ID NO:1 and a segment corresponding to the 119,670th to 119,683rd nucleotides of the antisense strand of the genomic DNA of the Dumas strain. Therefore, taking into consideration the difference between the parental Oka strain and the attenuated Oka strain, it became apparent that the deletion with respect to segments ATATATATA at the 3' end is useful for the quality control of a vaccine.

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Table 4

5		110087	
	D	GTACGCCAATCGGATACACTCTTTTGATCT	
	P	GTACGCCAATCGGATACACTCTTTTAATCT	
	V	GTACGCCAATCGGATACACTCTTTTAATCT	
10		110117	
	D	GCATTCGCACCTTCCCGTTTTTTCACGTAT	
	P	GCATTCGCACCTTCCCGTTTTTTCACGTAT	
	V	GCATTCGCACCTTCCCGTTTTTTCACGTAT	
15		110147	
	D	GGGTTTTCATTGTTTTGGCATGTGTCCAACC	
	P	GGGTTTTCATTGTTTTGGCATGTGTCCAACC	
	V	GGGTTTTCATTGTTTTGGCATGTGTCCAACC	
20		110177	
	D	ACCGTTCGCACCTTCTTTCTATATATATAT	
	P	ACCGTTCGCACCTTCTTTCTATATATATAT	
	V	ACCGTTCGCACCTTCTTTCTATATATATAT	
25		110207	
	D	ATATATATATATATATATATATAGAGAAAGAG	
	P	ATATATATATATA - - - - - GAGAGAGAG	
	V	ATATATA - - - - - GAGAGAGAG	
30		110237	
	D	AGAGAG - - - - - TTTCTTGTTTC	
	P	AGAGAGAGAGAGGGAGAGAGTTTCTTGTTTC	
	V	AGAGAGAGA - - GGGAGAGAGTTTCTTGTTTC	
35		110267	
	D	GCGCGTGTTCCCGCGATGTCGCGGTTTTAT	
	P	GCGCGTGTTCCCGCGATGTCGCGGTTTTAT	
	V	GCGCGTGTTCCCGCGATGTCGCGGTTTTAT	
40		110297	
	D	GGGGTGTTGGGCGGGCTTTTCACAGAATATA	
	P	GGGGTGTTGGGCGGGCTTTTCACAGAATATA	
	V	GGGGTGTTGGGCGGGCTTTTCACAGAATATA	
45		110327	
	D	TATATTCCAAATGGAGCGGCAGGCTTTTTA	
	P	TATATTCCAAATGGAGCGGCAGGCTTTTTA	
	V	TATATTCCAAATGGAGCGGCAGGCTTTTTA	
50		110357	
	D	AAATCGATT	D: Dumas strain
	P	AAATCGATT	P: Parental Oka strain
	V	AAATCGATT	V: Attenuated Oka strain

[0040] Table 5 shows the sequence alignment of the repetitive region R1 (in the direction of from the 5' end to the 3' end) of gene 11 of the Dumas strain, the parental Oka strain and the attenuated Oka strain.

[0041] Table 6 shows the sequence alignment of the repetitive region R3 (in the direction of from the 5' end to the 3' end) of gene 22 of the Dumas strain, the parental Oka strain and the attenuated Oka strain.

[0042] Table 7 shows the sequence alignment of the repetitive region R4 (in the direction of from the 5' end to the 3' end) of the Dumas strain, the parental Oka strain and the attenuated Oka strain.

[0043] As shown in Table 5, the repetitive sequences of whole R1 region of all three strains, namely the attenuated

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Oka strain, the parental Oka strain and the Dumas strain, are different from each other. Similarly, the repetitive sequences of whole R4 region of all three strains, namely the attenuated Oka strain, the parental Oka strain and the Dumas strain, are different from each other. Therefore, the repetitive sequence *abbabba'bbb'abababx* of R1 region (wherein, a represents a nucleotide sequence of GGACGCGATCGACGACGA; a' represents a nucleotide sequence of GGACGCGATTGACGACGA; b represents a nucleotide sequence of GGGAGAGGCGGAGGA; b' represents a nucleotide sequence of GGACGCGGCGGAGGA; and x represents a nucleotide sequence of GGA) and the repetitive sequence *aaaaaaaaaax* of R4 region (wherein, a represents a nucleotide sequence of CCCC GCCGATGGGGAGGGGCGCGGTA; and x represents a nucleotide sequence of CCCC GCCGATG) are unique to the attenuated varicella virus, and these sequences are useful for the quality control of an attenuated varicella live vaccine.

[0044] With respect to the sequences of the repetitive region R3 of gene 22 which are shown in Table 6, the sequences were diverse among the clones of the attenuated Oka strain and the parental Oka strain. Therefore, no unique sequence was found in the attenuated Oka strain.

Table 5
R1 region (gene 11)

Attenuated Oka strain	<i>abbabba'bbb'abababx</i>
Parental Oka strain	<i>abbabba'bbb'ababx</i>
Dumas strain	<i>abbabba'bba'bbbbabb'abx</i>
a:	GGACGCGATCGACGACGA
a':	GGACGCGATTGACGACGA
b:	GGGAGAGGCGGAGGA
b':	GGACGCGGCGGAGGA
x:	GGA

Table 6
R3 region (gene 22)

Attenuated Oka strain	
clone 1	<i>b'b'ab'b'ab'b'ab'ab'ab'ax</i>
clone 2	<i>b'b'ab'aab'ab'ax</i>
clone 3	<i>b'b'ab'aab'ab'ax</i>
clone 4	<i>b'b'ab'aab'ab'ax</i>
clone 5	<i>b'b'ab'ab'b'ab'ax</i>
clone 6	<i>b'b'ab'aab'ax</i>
clone 7	<i>b'b'ab' ax</i>
clone 8	<i>b'b'ab'ax</i>
clone 9	<i>b'b'ax</i>
clone 10	<i>b'b'ax</i>
Parental Oka strain	
clone 1	<i>b'b'ab'aab'ab'ax</i>
clone 2	<i>b'b'ab'aab'ax</i>
clone 3	<i>b'b'ab'ab'ax</i>
clone 4	<i>b'b'ab'ax</i>
clone 5	<i>b'b'ab'ax</i>
clone 6	<i>b'b'ab'ax</i>
clone 7	<i>b'b'ab'ax</i>
clone 8	<i>b'b'ax</i>
clone 9	<i>b'b'ax</i>

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(continued)

Parental Oka strain
Dumas strain aaaaabax

a: GCCCGCGCA
b: GACCGTCCA
b': GCCCGTCCA
x: GGA

Table 7
R4 region (noncoding region)

Attenuated Oka strain	aaaaaaaaaax
Parental Oka strain	aaaaaaaaaax
Dumas strain	aaaaax
a:	CCCGCCGATGGGGAGGGGGCGCGGTA
x:	CCCGCCGATG

Example 2

[0045] The genomic DNA of each of the attenuated Oka strain, the parental Oka strain and the Kawaguchi strain (wild-type strain of a varicella virus) was individually prepared in the same manner as in Example 1.

[0046] Using the PCR primers 01-N12 (SEQ ID NO:5) and 01-R13 (SEQ ID NO:6) shown in Table 8, a region corresponding to a part of gene 6 (a region corresponding to the 5,372nd to 6,134th nucleotides of the Dumas strain) was amplified by PCR, thereby obtaining a PCR product. The obtained PCR product (763 bp) was digested with the restriction enzyme Alu I to thereby cleave the DNA into fragments, and the restriction-fragment pattern was determined by an RFLP analysis. Specifically, each of the PCR products of the attenuated Oka strain, the parental Oka strain and the Kawaguchi strain was digested with the restriction enzyme Alu I, thereby obtaining a DNA fragment mixture, and the obtained DNA fragment mixture was applied to 4.0 % (w/v) agarose gel electrophoresis to determine the size of each DNA fragment.

[0047] Two fragments individually having a size of 170 bp and 593 bp were detected for the attenuated Oka strain. On the other hand, three fragments individually having a size of 170 bp, 205 bp and 388 bp were detected for the parental Oka strain and the Kawaguchi strain. These results show that the parental Oka strain and the Kawaguchi strain have the Alu I site located between the 205 bp fragment and the 388 bp fragment, but the attenuated Oka strain does not have this restriction site. It was confirmed from these results that the mutation of the 5,745th nucleotide A in gene 6 can be confirmed by detecting the absence of the Alu I site.

Example 3

[0048] 54 epidemic varicella strains derived from the varicella patients and the zoster patients were individually subjected to an RFLP analysis. Specifically, the difference in a restriction-fragment pattern obtained by digesting a PCR product with the restriction enzyme Alu I was determined by an RFLP analysis in the same manner as in Example 2. As a result, it was found that the PCR products of all epidemic strains were cleaved into three fragments individually having a size of 170 bp, 205 bp and 388 bp. Such a restriction-fragment pattern was the same as that of the parental Oka strain obtained in Example 2 above.

Example 4

[0049] The primers shown in Table 8 (SEQ ID NOs: 3 to 6 and 9 to 18) and the restriction enzymes Nla III, Alu I, Bst X I, Sfa I, Acc II, Sac II, Sma I, a combination of Bss H II and Nae I, or Bsr I were used to conduct an RFLP analysis in the same manner as in Example 2. Specifically, the genomic DNAs of each of the attenuated Oka strain, the parental Oka strain and the Kawaguchi strain were individually prepared in the same manner as in Example 1. Next, a specific region of the genomic DNA was amplified using the PCR primers shown in Table 8 in a specific combination shown in Table 9. The resultant PCR product was digested with a restriction enzyme and applied to an agarose gel electrophoresis. The results are shown in Fig. 2. In addition, the restriction enzymes used for the RFLP analysis and the sizes of the restriction fragments are summarized in Table 9.

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[0050] As is shown in Fig. 2 and Table 9, it became apparent that the numbers and sizes of the fragments resulting from the digestion of a PCR product of the attenuated Oka strain were different from those of the parental Oka strain and the Kawaguchi strain under all of the specific conditions employed for the RFLP analyses. Therefore, with respect to the 560th C, the 5,745th G, the 94,167th C, the 105,356th C (the 124,541st G), the 105,544th G (the 124,353rd C), the 105,705th C (the 124,192nd G), the 106,262nd C (the 123,635th G), the 107,136th C (the 122,761st G), the 107,252nd C (the 122,645th G), and the 108,111st C (the 121,786th G), the nucleotide mutations can be confirmed by an RFLP analysis without determining the nucleotide sequence of the genome.

Table 8

Primer	Nucleotide sequence	Nucleotide No.	
01-N01	5'-TCGTTTACTGCTCGGATGGCGACCG-3'	158-172	
01-R02	5'-GTGTTTATGTATCAGCATACAGAGC-3'	849-825	
01-N12	5'-ATTGTATGCATGCGATTGCTATCGC-3'	5372-5396	
01-R13	5'-GGTCTTCCACTTTAAAGGGGTTTGC-3'	6134-6110	
10-N29A	5'-GAATCATTAGTATATATTTTTCTGC-3'	26025-26049	
10-R30	5'-TGTTTCAGAGGGGATGAATCGTTGCG-3'	26165-26141	
50-N15	5'-CGATCACGTCGCTCACATCCAACCC-3'	93685-93709	
50-R17	5'-ATGGCAGAAGAAACACGTATTGCCG-3'	64457-64433	
60-N06	5'-GAGGACAACAGCTCCACCTTGACCG-3'	105277-105301	124620-124596
60-R06	5'-GAGTAATGTGGCCGCCCGTTTGG-3'	105613-105589	124284-124308
60-N26	5'-CCAAAACCGGGCGGCCACATTACTC-3'	105589-105613	124308-124284
60-R28	5'-ATTACTGTCGACCCGAGACCTGGCC-3'	106380-106356	123517-123541
G62-N04	5'-GATCAAAGCTTAGCGCAG-3'	106736-106753	123161-123144
G62-R04	5'-CCTATAGCATGGCTCCAG-3'	107499-107482	122398-122415
60-N11	5'-AAGGGCTTCCGTCGGGCATCATGAG-3'	107729-107753	122168-122144
60-R12	5'-TCGGGTAAAAAGCCGGCGATGAGC-3'	108497-108473	121400-121424

Table 9

PCR primer	Amplified fragmentary region (nucleotide no.)	Restriction enzyme	Restriction site (nucleotide no.)		Detected mutation (nucleotide no.)	Size of restriction fragment (bp)
01-N01 01-R02	158-849	<u>Nla</u> III	560		560	V 692 W 402 + 290
01-N12 01-R13	5372-6134	<u>Alu</u> I	5542 5747		5745	V 170 + 593 W 170 + 205 + 388
10-N29R 10-R30	26025-26165	<u>Mae</u> II	26125 26131		26125	V 100+6+35 W 100 + 35
50-N15 50-R17	93685-94457	<u>Bst</u> X I	94172		94167	V 487 + 286 W 773
		<u>Sfa</u> N I	105347	124550	105356 124541	V 337 W 70 + 267

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(continued)

5	PCR primer	Amplified fragmentary region (nucleotide no.)	Restriction enzyme	Restriction site (nucleotide no.)		Detected mutation (nucleotide no.)	Size of restriction fragment (bp)
	60-N06	105277-105613					
	60-R06	124284-124620		105422	124475		V 145 + 162 + 39 + 30
10			<u>Acc II</u>	105545	124352	105544	
				105584	124313	124353	W 145 + 162 + 30
				105707	124190	105705	V 118 + 338 + 336
15			<u>Sac II</u>	106045	123852	124192	W 456 + 336
	60-N26	105589-106380					
	60-R28	123517-124308		106072	123825		V 483 + 79 + 112 + 118
20			<u>Sma I</u>	106151	123746	106262	
				106263	123634	123635	W 483 + 79 + 230
						107136	
25			<u>BssH II</u>	107136	122761	122761	
	G62-N04	106736-107499					V 400 + 117 + 247
	G62-R04	122398-123161					W 764
30			<u>Nae I</u>	107252	122645	107252	
						122645	
	60-N11	107729-108497				108111	V 769
	60-R12	121400-122168	<u>Bsr I</u>	108113	121784	121786	W 384 + 385
35	V: Attenuated Oka strain W: Wild-type strain (Virulent strain)						

INDUSTRIAL APPLICABILITY

40 [0051] According to the method for quality control of the present invention, it has become possible to conduct an exact quality control and quality assurance of an attenuated varicella live vaccines, particularly with respect to the safety, effectiveness and uniformity of the vaccine. Further, the present invention provides exact and advantageous techniques which can be used for research in the field of epidemiology of varicella and zoster, including a tracing of the effects of vaccination, and these techniques may expedite and enhance the research. Consequently, the present invention provides
45 an exact and very effective measure for preventing varicella and zoster, which contributes to the health of human beings.

SEQUENCE LISTING

50 [0052]

<110> The Research Foundation for Microbial Diseases of Osaka University

<120> Method for quality control of an attenuated varicella live vaccine

55 <130> JHB/100-1058/JLH

<140> PCT/JP01/00678

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<141> 2001-01-31

<150> JP 2000-62734

<151> 2000-01-31

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<212> DNA

<213> Varicella virus Dumas strain

<400> 1

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65 <210> 10
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 <210> 14
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 40 <212> DNA
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 <220>
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122645th and 122761st nucleotides of a varicella vaccine virus

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<210> 16

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<212> DNA

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<210> 17

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<212> DNA

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<223> Description of Artificial Sequence: PCR primer used for detecting mutations of the 108111st and 121786th nucleotides of a varicella vaccine virus

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<210> 18

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<212> DNA

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<223> Description of Artificial Sequence: PCR primer used for detecting mutations of the 108111st and 121786th nucleotides of a varicella vaccine virus

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Claims

1. A method for the quality control of an attenuated varicella live vaccine, which comprises subjecting the genomic DNA of a sample varicella vaccine virus to sequence analysis and confirming that the genomic DNA of said sample varicella vaccine virus conserves without suffering mutation the following 5 nucleotides:

the 5,745th G, the 105,356th C, the 105,544th G, the 106,262nd C and the 107,252nd C,

wherein the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

2. The method according to claim 1, wherein the conservation of said 5 nucleotides combination is confirmed by an RFLP analysis using the following primers:

a pair of primers of SEQ ID NOs: 5 and 6 with respect to the confirmation of the 5,745th G;

a pair of primers of SEQ ID NOs: 11 and 12 with respect to the confirmation of the 105,356th C and the 105,544th

G;
a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 106,262nd C; and
a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 107,252nd C.

- 5 3. The method according to claim 1 or 2, which further comprises confirming that the genomic DNA of said sample varicella vaccine virus conserves without suffering mutation the following 4 nucleotides:

the 122,645th G, the 123,635th G, the 124,353rd C and the 124,541st G,

10 wherein the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

4. The method according to claim 3, wherein the conservation of said 4 nucleotides is confirmed by an RFLP analysis using the following primers:

15 a pair of primers of SEQ ID NOs: 11 and 12 with respect to the confirmation of the 124,353rd C and the 124,541st G;
a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 123,635th G; and
a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 122,645th G.

- 20 5. The method according to any one of claims 1 to 4, which further comprises confirming that the genomic DNA of said sample varicella vaccine virus conserves without suffering mutation the following 49 nucleotides:

25 the 560th C, the 703rd Y, the 763rd Y, the 2,515th Y, the 10,900th Y, the 12,779th Y, the 19,431st Y, the 26,125th G, the 31,732nd Y, the 38,036th Y, the 39,227th K, the 58,595th R, the 59,287th R, the 64,067th R, the 71,252nd Y, the 82,225th R, the 84,091st R, the 87,280th R, the 87,306th Y, the 89,734th R, the 90,535th R, the 94,167th C, the 97,748th R, the 97,796th Y, the 101,089th R, the 105,169th R, the 105,310th R, the 105,705th C, the 106,710th R, the 107,136th C, the 107,599th R, the 107,797th R, the 108,111st C, the 108,838th R, the 109,137th R, the 109,200th R, the 111,650th R, the 118,247th Y, the 120,697th Y, the 120,760th Y, the 121,059th Y, the 121,786th G, the 122,100th Y, the 122,298th Y, the 122,761st G, the 123,187th Y, the 124,192nd G, the 124,587th Y and the 124,728th Y,

wherein:

35 the nucleotide numbers are in accordance with the nucleotide numbering system of the nucleotide sequence of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1,
R represents A or G,
Y represents C or T, and
K represents G or T.

- 40 6. The method according to claim 5, wherein the conservation of the 560th C, the 26,125th G, the 94,167th C, the 105,705th C, the 107,136th C, the 108,111st C, the 121,786th G, the 122,761st G and the 124,192nd G among said 49 nucleotides is confirmed by an RFLP analysis using the following primers:

45 a pair of primers of SEQ ID NOs: 3 and 4 with respect to the confirmation of the 560th C;
a pair of primers of SEQ ID NOs: 7 and 8 with respect to the confirmation of the 26,125th G;
a pair of primers of SEQ ID NOs: 9 and 10 with respect to the confirmation of the 94,167th C;
a pair of primers of SEQ ID NOs: 13 and 14 with respect to the confirmation of the 105,705th C and the 124,192nd G;
50 a pair of primers of SEQ ID NOs: 15 and 16 with respect to the confirmation of the 107,136th C and the 122,761st G; and
a pair of primers of SEQ ID NOs: 17 and 18 with respect to the confirmation of the 108,111st C and the 121,786th G.

- 55 7. The method according to any one of claims 1 to 6, which further comprises confirming deletion mutations in two origins of replication of the genomic DNA of said sample varicella vaccine virus,
wherein said two origins of replication are a region corresponding to the 110,087th to 110,350th nucleotides of the sense strand of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1 and a region corresponding

to the 119,547th to 119,810th nucleotides of the genomic DNA of the antisense strand of said Dumas strain, and wherein said deletion mutations occur with respect to segments each having a nucleotide sequence of ATATATATA arranged in the direction of from the 5' end to the 3' end, said segments being a segment corresponding to the 110,219th to 110,227th nucleotides of the sense strand of the genomic DNA of said Dumas strain and a segment corresponding to the 119,670th to 119,678th nucleotides of the antisense strand of the genomic DNA of said Dumas strain.

8. The method according to any one of claims 1 to 7, which further comprises confirming that the repetitive sequence of one whole R1 region of the genomic DNA of said sample varicella vaccine virus is a nucleotide sequence of abbabba'bbb'abababx arranged in the direction of from the 5' end to the 3' end, wherein:

a represents a nucleotide sequence of

GGACGCGATCGACGACGA;

a' represents a nucleotide sequence of

GGACGCGATTGACGACGA;

b represents a nucleotide sequence of

GGGAGAGGCGGAGGA;

b' represents a nucleotide sequence of GGACGCGGCGGAGGA; and

x represents a nucleotide sequence of GGA,

wherein said whole R1 region is a region corresponding to the 13,937th to 14,242nd nucleotides of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1.

9. The method according to any one of claims 1 to 8, which further comprises confirming that the repetitive sequence of each of two whole R4 regions of the genomic DNA of said sample varicella vaccine virus is a nucleotide sequence of aaaaaaaaaaax arranged in the direction of from the 5' end to the 3' end, wherein:

a represents a nucleotide sequence of

CCCCGCCGATGGGGAGGGGGCGCGGTA; and

x represents a nucleotide sequence of

CCCCGCCGATG,

wherein said two whole R4 regions are a region corresponding to the 109,762nd to 109,907th nucleotides of the sense strand of the genomic DNA of the varicella virus Dumas strain of SEQ ID NO: 1 and a region corresponding to the 119,990th to 120,135th nucleotides of the antisense strand of the genomic DNA of said Dumas strain.

Patentansprüche

1. Verfahren zur Qualitätskontrolle eines abgeschwächten Varicella-Lebendimpfstoffs, umfassend das Durchführen einer Sequenzanalyse mit der genomischen DNA einer Probe des Varicella-Impfstoffvirus und Bestätigen, dass die genomische DNA der Probe des Varicella-Impfstoffvirus die folgenden 5 Nucleotide ohne Mutation konserviert:

das 5745. G, das 105356. C, das 105544. G, das 106262. C und das 107252. C;

wobei die Nucleotidnummern dem Nucleotidnummerierungssystem der Nucleotidsequenz der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entsprechen.

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2. Verfahren gemäß Anspruch 1, wobei die Konservierung der Kombination von 5 Nucleotiden durch eine RFLP-Analyse unter Verwendung der folgenden Primer bestätigt wird:

ein Paar von Primern der SEQ ID Nr. 5 und 6 zur Bestätigung des 5745. G;
ein Paar von Primern der SEQ ID Nr. 11 und 12 zur Bestätigung des 105356. C und des 105544. G;
ein Paar von Primern der SEQ ID Nr. 13 und 14 zur Bestätigung des 106262. C; und
ein Paar von Primern der SEQ ID Nr. 15 und 16 zur Bestätigung des 107252. C.

3. Verfahren gemäß Anspruch 1 oder 2, das weiterhin Folgendes umfasst:

Bestätigen, dass die genomische DNA der Probe des Varicella-Impfstoffvirus die folgenden 4 Nucleotide ohne Mutation konserviert:

das 122645. G, das 123635. G, das 124353. C und das 124541. G;

wobei die Nucleotidnummern dem Nucleotidnummerierungssystem der Nucleotidsequenz der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entsprechen.

4. Verfahren gemäß Anspruch 3, wobei die Konservierung der 4 Nucleotide durch eine RFLP-Analyse unter Verwendung der folgenden Primer bestätigt wird:

ein Paar von Primern der SEQ ID Nr. 11 und 12 zur Bestätigung des 124353. C und des 124541. G;
ein Paar von Primern der SEQ ID Nr. 13 und 14 zur Bestätigung des 123635. G; und
ein Paar von Primern der SEQ ID Nr. 15 und 16 zur Bestätigung des 122645. G.

5. Verfahren gemäß einem der Ansprüche 1 bis 4, das weiterhin Folgendes umfasst: Bestätigen, dass die genomische DNA der Probe des Varicella-Impfstoffvirus die folgenden 49 Nucleotide ohne Mutation konserviert:

das 560. C, das 703. Y, das 763. Y, das 2,515. Y, das 10,900. Y, das 12,779. Y, das 19,431. Y, das 26,125. G, das 31,732. Y, das 38,036. Y, das 39,227. K, das 58,595. R, das 59,287. R, das 64,067. R, das 71,252. Y, das 82,225. R, das 84,091. R, das 87,280. R, das 87,306. Y, das 89,734. R, das 90,535. R, das 94,167. C, das 97,748. R, das 97,796. Y, das 101,089. R, das 105,169. R, das 105,310. R, das 105,705. C, das 106,710. R, das 107,136. C, das 107,599. R, das 107,797. R, das 108,111. C, das 108,838. R, das 109,137. R, das 109,200. R, das 111,650. R, das 118,247. Y, das 120,697. Y, das 120,760. Y, das 121,059. Y, das 121,786. G, das 122,100. Y, das 122,298. Y, das 122,761. G, das 123,187. Y, das 124,192. G, das 124,587. Y und das 124,728. Y;

wobei die Nucleotidnummern dem Nucleotidnummerierungssystem der Nucleotidsequenz der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entsprechen;

R für A oder G steht;

Y für C oder T steht; und

K für G oder T steht.

6. Verfahren gemäß Anspruch 5, wobei die Konservierung des 560. C, des 26,125. G, des 94,167. C, des 105,705. C, des 107,136. C, des 108,111. C, des 121,786. G, des 122,761. G und des 124,192. G unter den 49 Nucleotiden durch eine RFLP-Analyse unter Verwendung der folgenden Primer bestätigt wird:

ein Paar von Primern der SEQ ID Nr. 3 und 4 zur Bestätigung des 560. C;
ein Paar von Primern der SEQ ID Nr. 7 und 8 zur Bestätigung des 26,125. G;
ein Paar von Primern der SEQ ID Nr. 9 und 10 zur Bestätigung des 94,167. C;
ein Paar von Primern der SEQ ID Nr. 13 und 14 zur Bestätigung des 105,705. C und des 124,192. G;
ein Paar von Primern der SEQ ID Nr. 15 und 16 zur Bestätigung des 107,136. C und des 122,761. G; und
ein Paar von Primern der SEQ ID Nr. 17 und 18 zur Bestätigung des 108,111. C und des 121,786. G.

7. Verfahren gemäß einem der Ansprüche 1 bis 6, das weiterhin Folgendes umfasst: Bestätigen von Deletionsmutationen in zwei Replikationsstartpunkten der genomischen DNA der Probe des Varicella-Impfstoffvirus; wobei die zwei Replikationsstartpunkte einen Bereich, der dem 110087. bis 110350. Nucleotid des Sense-Strangs der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entspricht, bzw. einen Bereich, der dem 119547. bis 119810. Nucleotid der genomischen DNA des Antisense-Strangs des genannten Dumas-Stamms

entspricht, bilden; und

wobei die Deletionsmutationen in Bezug auf Segmente stattfinden, die jeweils die Nucleotidsequenz ATATATATA aufweisen, die in Richtung vom 5'-Ende zum 3'-Ende angeordnet ist, wobei es sich bei den Segmenten um ein Segment, das dem 110219. bis 110227. Nucleotid des Sense-Strangs der genomischen DNA des genannten Dumas-Stamms entspricht, und ein Segment, das dem 119670. bis 119678. Nucleotid des Antisense-Strangs der genomischen DNA des genannten Dumas-Stamms entspricht, handelt.

8. Verfahren gemäß einem der Ansprüche 1 bis 7, das weiterhin Folgendes umfasst: Bestätigen, dass die repetitive Sequenz eines ganzen R1-Bereichs der genomischen DNA der Probe des Varicella-Impfstoffvirus die Nucleotidsequenz abbabba'bbb'abababx ist, die in Richtung vom 5'-Ende zum 3'-Ende angeordnet ist; wobei a der Nucleotidsequenz

GGACGCGATCGACGACGA

entspricht, a' der Nucleotidsequenz

GGACGCGATTGACGACGA

entspricht, b der Nucleotidsequenz

GGGAGAGGCGGAGGA

entspricht, b' der Nucleotidsequenz

GGACGCGGCGGAGGA

entspricht und x der Nucleotidsequenz GGA entspricht,

wobei der ganze R1-Bereich ein Bereich ist, der dem 13937. bis 14242. Nucleotid der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entspricht.

9. Verfahren gemäß einem der Ansprüche 1 bis 8, das weiterhin Folgendes umfasst: Bestätigen, dass die repetitive Sequenz jedes der beiden ganzen R4-Bereiche der genomischen DNA der Probe des Varicella-Impfstoffvirus die Nucleotidsequenz aaaaaaaaaaax ist, die in Richtung vom 5'-Ende zum 3'-Ende angeordnet ist; wobei a der Nucleotidsequenz

CCCCGCCGATGGGGAGGGGGCGCGGTA

entspricht und x der Nucleotidsequenz

CCCCGCCGATG

entspricht;

wobei es sich bei den beiden ganzen R4-Bereichen um einen Bereich, der dem 109762. bis 109907. Nucleotid des Sense-Strangs der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entspricht, und einen Bereich, der dem 119990. bis 120135. Nucleotid des Antisense-Strangs der genomischen DNA des Varicellavirus-Dumas-Stamms der SEQ ID Nr. 1 entspricht, handelt.

Revendications

1. Procédé pour régler la qualité d'un vaccin de virus vivant de varicelle atténuée, dans lequel on soumet l'ADN génomique d'un virus de vaccin de varicelle échantillon à une analyse de séquence et on confirme que l'ADN génomique du virus de vaccin de varicelle échantillon conserve, sans souffrir de mutation, les cinq nucléotides suivants :

le 5 745ème G, le 105 356ème C, le 105 544ème G, le 106 262ème C et le 107 252ème C, les numéros des nucléotides étant conformes au système de numérotation des nucléotides de la séquence de nucléotides de l'ADN génomique de la souche Dumas de virus de la varicelle ayant l'identification de séquence

n° 1.

2. Procédé suivant la revendication 1, dans lequel on confirme la conservation de la combinaison de 5 nucléotides par une analyse RFLP en utilisant les amorces suivantes :

une paire d'amorces d'identification de séquences n° 5 et 6 pour ce qui concerne la confirmation du 5 745ème G ;
une paire d'amorces d'identification de séquences n° 11 et 12 pour ce qui concerne la confirmation du 105 356ème C et du 105 544ème G ;
une paire d'amorces d'identification de séquences n° 13 et 14 pour ce qui concerne la confirmation du 106 262ème C ;
et
une paire d'amorces d'identification de séquences n° 15 et 16 pour ce qui concerne la confirmation du 107 252ème C.

3. Procédé suivant la revendication 1 ou 2, qui comprend en outre la confirmation que l'ADN génomique du virus de vaccin de varicelle échantillon conserve, sans souffrir de mutation, les 4 nucléotides suivants :

le 122 645ème G, le 123 635ème G, le 124 353ème C et le 124 541ème G,
les numéros des nucléotides étant conformes au système de numérotation des nucléotides de la séquence de nucléotides de l'ADN génomique de la souche Dumas de virus de la varicelle ayant l'identification de séquence n° 1.

4. Procédé suivant la revendication 3, dans lequel on confirme la conservation des 4 nucléotides par une analyse RFLP en utilisant les amorces suivantes :

une paire d'amorces d'identification de séquences n° 11 et 12 pour ce qui concerne la confirmation du 124 353ème C et du 124 541ème G ;
une paire d'amorces d'identification de séquences n° 13 et 14 pour ce qui concerne la confirmation du 123 635ème G ;
et
une paire d'amorces d'identification de séquences n° 15 et 16 pour ce qui concerne la confirmation du 122 645ème G.

5. Procédé suivant l'une quelconque des revendications 1 à 4, qui comprend en outre la confirmation que l'ADN génomique du virus de vaccin de varicelle échantillon conserve, sans souffrir de mutation, les 49 nucléotides suivants :

le 560ème C, le 703ème Y, le 763ème Y, le 2 515ème Y, le 10 900ème Y, le 12 779ème Y, le 19 431ème Y, le 26 125ème G, le 31 732ème Y, le 38 036ème Y, le 39 227ème K, le 58 595ème R, le 59 287ème R, le 64 067ème R, le 71 252ème Y, le 82 225ème R, le 84 091ème R, le 87 280ème R, le 87 306ème Y, le 89 734ème R, le 90 535ème R, le 94 167ème C, le 97 748ème R, le 97 796ème Y, le 101 089ème R, le 105 169ème R, le 105 310ème R, le 105 705ème C, le 106 710ème R, le 107 136ème C, le 107 599ème R, le 107 797ème R, le 108 111ème C, le 108 838ème R, le 109 137ème R, le 109 200ème R, le 111 650ème R, le 118 247ème Y, le 120 697ème Y, le 120 760ème Y, le 121 059ème Y, le 121 786ème G, le 122 100ème Y, le 122 298ème Y, le 122 761ème G, le 123 187ème Y, le 124 192ème G, le 124 587ème Y et le 124 728ème Y,

dans lequel :

les numéros des nucléotides étant conformes au système de numérotation des nucléotides de la séquence de nucléotides de l'ADN génomique de la souche Dumas de virus de la varicelle ayant l'identification de séquence n° 1,
R représente A ou G,
Y représente C ou T, et
K représente G ou T.

6. Procédé suivant la revendication 5, dans lequel on confirme la conservation du 560ème C, du 26 125ème G, du 94 167ème C, du 105 705ème C, du 107 136ème C, du 108 111ème C, du 121 786ème G, du 122 761ème G et du 124 192ème G parmi les 49 nucléotides par une analyse RFLP en utilisant les amorces suivantes :

une paire d'amorces d'identification de séquences n° 3 et 4 pour ce qui concerne la confirmation du 560ème C ;
une paire d'amorces d'identification de séquences n° 7 et 8 pour ce qui concerne la confirmation du 26 125ème G ;
une paire d'amorces d'identification de séquences n° 9 et 10 pour ce qui concerne la confirmation du 94 167ème C ;

une paire d'amorces d'identification de séquences n° 13 et 14 pour ce qui concerne la confirmation du 105 705ème C et du 124 192ème G ;

une paire d'amorces d'identification de séquences n° 15 et 16 pour ce qui concerne la confirmation du 107 136ème C et du 122 761ème G ; et

une paire d'amorces d'identification de séquences n° 17 et 18 pour ce qui concerne la confirmation du 108 111ème C et du 121 786ème G.

7. Procédé suivant l'une quelconque des revendications 1 à 6, qui comprend en outre la confirmation de mutations de délétion dans deux origines de réplication de l'ADN génomique du virus de vaccin de varicelle échantillon, dans lequel deux origines de réplication sont une région allant du 110 087ème au 110 350ème nucléotides du brin signifiant de l'ADN génomique de la souche de Dumas du virus de la varicelle ayant l'identification de séquence n° 1 et une région allant du 119 547ème au 119 810ème nucléotides de l'ADN génomique du brin antisens de la souche de Dumas, et dans lequel des mutations par délétion se produisent par rapport à des segments ayant chacun une séquence de nucléotides constituée de ATATATATA, disposée dans le sens allant de l'extrémité 5' à l'extrémité 3', les segments ayant un segment allant du 110 219ème au 110 227ème nucléotides du brin signifiant de l'ADN génomique de la souche de Dumas et un segment allant du 119 670ème au 119 678ème nucléotides du brin antisens de l'ADN génomique de la souche de Dumas.

8. Procédé suivant l'une quelconque des revendications 1 à 7, qui comprend en outre la confirmation que la séquence de répétition d'une région R1 complète de l'ADN génomique du virus du vaccin de la varicelle échantillon est une séquence de nucléotides de abbabba'bbb'abababx disposée dans le sens allant de l'extrémité 5' à l'extrémité 3', dans lequel :

a représente une séquence de nucléotides constituée de GGACGCGATCGACGACGA ;

a' représente une séquence de nucléotides constituée de GGACGCGATTGACGACGA ;

b représente une séquence de nucléotides constituée de GGGAGAGGCGGAGGA ;

b' représente une séquence de nucléotides constituée de GGACGCGGCGGAGGA ; et

x représente une séquence de nucléotides constituée de GGA,

dans lequel la région R1 complète est une région allant du 13 937ème au 14 242ème nucléotides de l'ADN génomique de la souche de Dumas du virus de la varicelle de l'identification de séquence n° 1.

9. Procédé suivant l'une quelconque des revendications 1 à 8, qui comprend en outre la confirmation que la séquence de répétition de chacune des deux régions R4 complètes de l'ADN génomique du virus de vaccin de varicelle échantillon est une séquence de nucléotides constituée de aaaaaaaaaaax, disposée dans le sens allant de l'extrémité 5' à l'extrémité 3', dans lequel :

a représente une séquence de nucléotides constituée de CCCC GCCGATG GGGAGGGGGCGCGGTA ; et

x représente une séquence de nucléotides constituée de CCCC GCCGATG,

dans lequel les deux régions R4 complètes sont une région allant du 109 762ème au 109 907ème nucléotides du brin signifiant de l'ADN génomique de la souche de Dumas du virus de varicelle de l'identification de séquence n° 1 et une région allant du 119 990ème au 120 135ème nucléotides du brin antisens de l'ADN génomique de la souche de Dumas.

Fi. 50

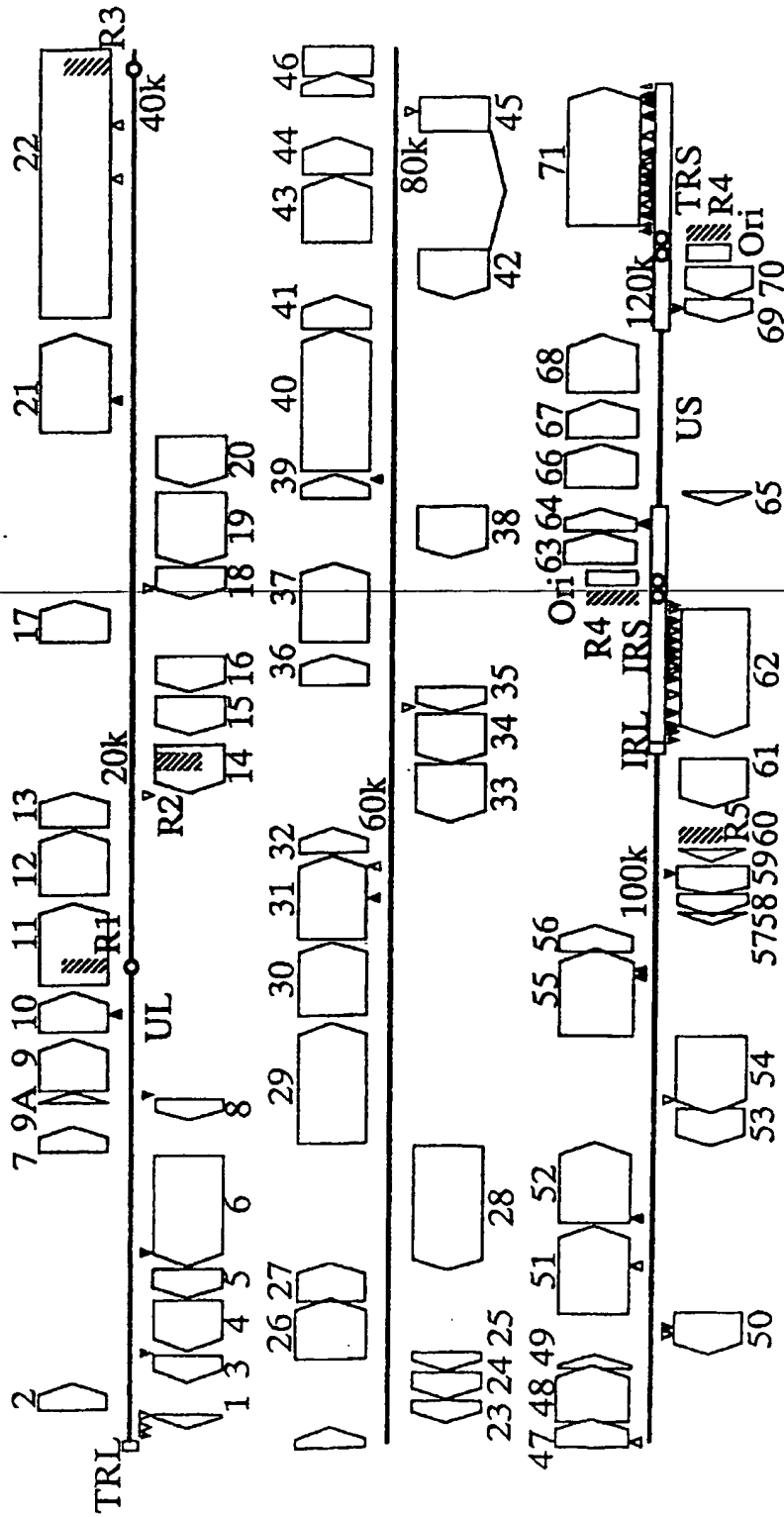
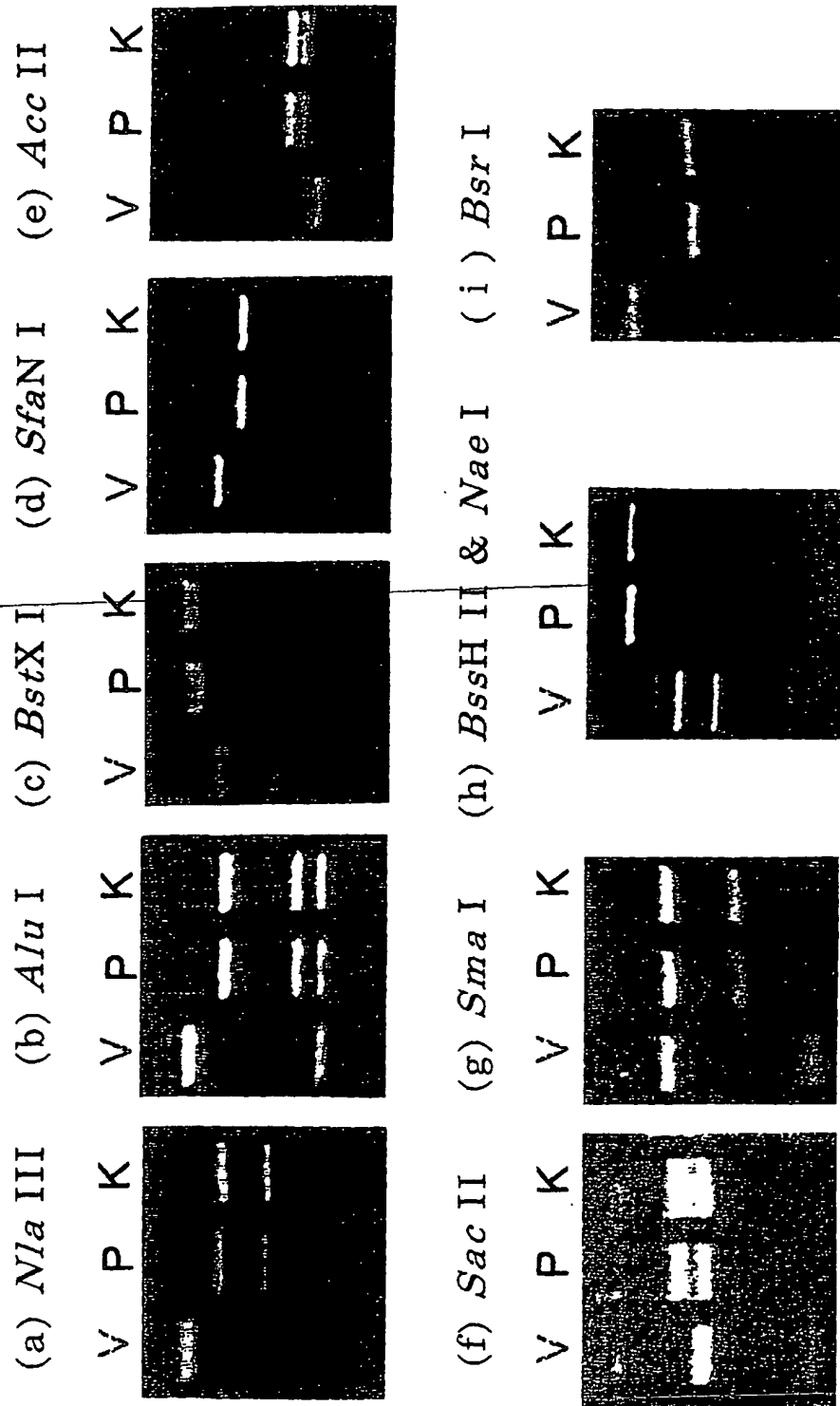


Fig. 2



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